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OM protein - protein search, using sw model

Run on: March 27, 2005, 20:32:06 ; Search time 54 Seconds  
(without alignments)  
1118.354 Million cell updates/sec

Title: US-09-855-828-1  
Perfect score: 4234  
Sequence: 1 MFKSLTKVKNKVPIGENNEN.....PSAEGGEVLTIEVKEKAQ 809

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Issued Patents AA.\*
- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pap.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pap.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pap.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pap.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pap.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3166.5	74.8	610	4	US-09-949-016-6945
2	2202	52.0	416	4	US-09-949-016-11669
3	1949	46.0	909	4	US-09-538-092-1315
4	857	20.2	698	4	US-09-949-016-10215
5	850	20.1	694	4	US-09-538-092-1351
6	818.5	19.3	690	4	US-09-275-252A-19
7	817	19.3	686	4	US-09-538-092-1037
8	817	19.3	694	4	US-09-949-016-11549
9	484	11.4	261	4	US-09-275-252A-18
10	416.5	9.8	256	4	US-09-270-767-46624
11	413	9.8	1203	4	US-09-949-016-6615
12	412.5	9.7	910	4	US-08-997-685A-6
13	412.5	9.7	910	4	US-09-086-436-31
14	412.5	9.7	1109	4	US-09-949-016-10771
15	405.5	9.6	889	4	US-09-949-016-6036
16	399.5	9.4	855	4	US-09-949-016-7263
17	382.5	9.0	749	4	US-08-997-685A-10
18	382.5	9.0	749	4	US-09-086-436-39
19	382	9.0	528	4	US-08-997-685A-4
20	377.5	8.9	504	4	US-09-086-436-33
21	370	8.7	597	4	US-08-997-685A-12
22	368	8.7	506	4	US-08-997-685A-6
23	368	8.7	506	4	US-09-086-436-35
24	368	8.7	597	4	US-09-086-436-41
25	360.5	8.5	960	4	US-09-694-777A-21
26	349	8.2	987	4	US-09-694-777A-22
27	347.5	8.2	962	4	US-09-694-777A-24

ALIGNMENTS

RESULT 1

US-09-949-016-6945  
; Sequence 6945, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6945  
; LENGTH: 610  
; TYPE: PRT  
; ORGANISM: Human  
; US-09-949-016-6945

Query Match 74.8%; Score 3166.5; DB 4; Length 610;  
Best Local Similarity 99.0%; Pred. No. 3.5e-273;  
Matches 609; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

Qy	195	MLPEYLKRIKLPNSIDSYTDRLYLLMLLVTLAYNNWCWFIPLRLVPPYQTAADNIHYWL	254
Db	1	MLPEYLKRIKLPNSIDSYTDRLYLLMLLVTLAYNNWCWFIPLRLVPPYQTAADNIHYWL	60
Qy	255	IADIICDIYLYDMFLTPQLRQFVRGGDIIVDSNELKRGHYRTSTKFDQDVASIIPFDICY	314
Db	61	IADIICDIYLYDMFLTPQLRQFVRGGDIIVDSNELKRGHYRTSTKFDQDVASIIPFDICY	120
Qy	315	LFPGFNPFRANRMLKYTSFPFNNHLESIMDKAYIYRVIRTTGYLLFILHINACVYWA	374
Db	121	LFPGFNPFRANRMLKYTSFPFNNHLESIMDKAYIYRVIRTTGYLLFILHINACVYWA	180
Qy	375	SNYEGIGTRRWYDGEYRCYVAVRTLTITGGLPPEPOTLFEIVFOLLNPFSGVVPF	434
Db	181	SNYEGIGTRRWYDGEYRCYVAVRTLTITGGLPPEPOTLFEIVFOLLNPFSGVVPF	240
Qy	435	SSLLGQMRDVIQATANQNYFRACMDDTIAYMNNYSIPKLQKRVRTWYETWDSQRMULD	494
Db	241	SSLLGQMRDVIQATANQNYFRACMDDTIAYMNNYSIPKLQKRVRTWYETWDSQRMULD	300
Qy	495	ESDLLKLTPTTVQLALAIQVNFISIISKVDLPKGCOTQMIYDMLRLKSVLYLPGDFVCKK	554

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Db 301 ESDLLKLTPTTVQALALDVNFSSIIISKVDLPFGKCDTQMIYDMLLRKSLVLYLPGDFVCKK 360
Qy 555 GEIGKEMYYIKHGEVOVLGGDGTGKVLVTLKAGSVFGEISLLAAGGNRRRTANVAHGFA 614
Db 361 GEIGKEMYYIKHGEVOVLGGDGTGKVLVTLKAGSV-----LLAAGGNRRRTANVAHGFA 415
Qy 615 NLLTLDKKTQLQEIILVHPDSEIRIIMKKARVLLKQAKTATPRKDLALLFPKERTPK 674
Db 416 NLLTLDKKTQLQEIILVHPDSEIRIIMKKARVLLKQAKTATPRKDLALLFPKERTPK 475
Qy 675 LFKTLGGTGKASLARLLKLKREQAAQKENSEGEEGKENEKDKENEDK 734
Db 476 LFKTLGGTGKASLARLLKLKREQAAQKENSEGEEGKENEKDKENEDK 535
Qy 735 KENEDKDKGPEKPLDRPECTASPIAVBEEPHSVRTVLPRTGTSQSIIISMASAE 794
Db 536 KENEDKDKGPEKPLDRPECTASPIAVBEEPHSVRTVLPRTGTSQSIIISMASAE 595
Qy 795 GEEVLTIEVKEKAQ 809
Db 596 GEEVLTIEVKEKAQ 610

RESULT 2
US-09-949-016-11669
; Sequence 11669, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11669
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11669

Query Match 52.0%; Score 2202; DB 4; Length 416;
Best Local Similarity 99.8%; Pred. No. 1.7e-187;
Matches 412; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 114 POKPAPVINEYADAQLHNLVKRMQRPTALYKXKLVEGDLSPEASPTAKPTAVPPV 173
Db 1 POKPAPVINEYADAQLHNLVKRMQRPTALYKXKLVEGDLSPEASPTAKPTAVPPV 60
Qy 174 KESDDKPTHEYRLHFWKVKMPLTEYLKIKLPNSDTSYDRLYLMLLVTLAYNWC 233
Db 61 KESDDKPTHEYRLHFWKVKMPLTEYLKIKLPNSDTSYDRLYLMLLVTLAYNWC 120
Qy 234 WFIPLRVFPYQADNIHNYLWLIADIICDIITYLDMLFQPRLOFVRGGDIIVDSNELRXH 293
Db 121 WFIPLRVFPYQADNIHNYLWLIADIICDIITYLDMLFQPRLOFVRGGDIIVDSNELRXH 180
Qy 294 YRTSTKQLDVASIIPFDICYLFFGNPMFRANMLKYTSFFPNHLSIMDKAYIYRV 353
Db 181 YRTSPKQLDVASIIPFDICYLFFGNPMFRANMLKYTSFFPNHLSIMDKAYIYRV 240
Qy 354 IRTTGVLFLTLHNACVYVWASVNEGIGTRRWYDGEHNYLRCYVWAVRTLITIGLPE 413
Db 241 IRTTGVLFLTLHNACVYVWASVNEGIGTRRWYDGEHNYLRCYVWAVRTLITIGLPE 300
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Qy 414 POTLFEIVFQLLNFFSGVFVSSLIQMRDVIKAATANQNYFRACMDDTIAYMNNYSIPK 473
Db 301 POTLFEIVFQLLNFFSGVFVSSLIQMRDVIKAATANQNYFRACMDDTIAYMNNYSIPK 360
Qy 474 LVQKRVRTWYETWDSQRMDESDDLKLTPTTVQALALDVNFSSIIISKVDLPK 526
Db 361 LVQKRVRTWYETWDSQRMDESDDLKLTPTTVQALALDVNFSSIIISKVDLPK 413

RESULT 3
US-09-538-092-1315
; Sequence 1315, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormat Version 0.9
; SEQ ID NO 1315
; LENGTH: 909
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)-(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14028
US-09-538-092-1315

Query Match 46.0%; Score 1949; DB 4; Length 909;
Best Local Similarity 46.2%; Pred. No. 2e-164;
Matches 403; Conservative 122; Mismatches 238; Indels 110; Gaps 18;

Qy 14 IGNNENEGSSRRNEGSHPSNQSOOTTAQE--ENKGE---EKSLKTKSTPVTSEPHTN 68
Db 67 VGEZAKKEAEKAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAE 126
Qy 69 IODK-----LSKKNSSGDLTTNPDQNAAEPTCTVPEQEMDPKGGPN----- 112
Db 127 VEDTDADSCPLMAENPPS--TVLPPSPAKSDTLIVPSSASGTHRKKLUPSEDDDAEELK 184
Qy 113 --SPQNKP-----PAAP-----VINEYADAQLHNLVKRMQRPTALY 146
Db 185 ALSPAESFVVAWSDDPTTKDTPGDRAASTASTNSAIIND---RLQELVKLFKERTKV 240
Qy 147 KKKLVEGDL-----SPEASPTAKPTAVPPVKESDDKPT--EHYRLLWFKVKKPLTEY 200
Db 241 KEKLIDPDVTSDEESPKSPAKAPAPDTKPAEAEVPEEHEHYCDMLCKCFKHPWKY 300
Qy 201 LKRIKLPNSIDSYDRLYLMLLVTLAYNWCWFIPLRVFPYQADNIHNYLWLIADIIC 260
Db 301 ----QFOSIDPLTNLMVTLWLFVVMANWNCWLIIPVRWAPPYOTPDNIHHLMDYLIC 356
Qy 261 DIYLYLDMFLIOPRLQFVRGGDIIVDSNELRKHRTSTKQLDVASIIPFDICYLFFGN 320
Db 357 DLIIYFLDITVFTRLQFVRGGDIITDKDMRNLYKSRFKMDLSLLPLDPLYLKVGW 416
Qy 321 PMFRANMLKYTSFFPNHLSIMDKAYIYRVITTTGTLFILHNACVYVWASVNEGIG 380
Db 417 PLLRLPRLCYMAFPEFNSRLESILSKAYVYRVIRTTAYLLYSLHNSCLYVWASVQGL 476
Qy 381 GTTRWYDGEHNYLRCYVWAVRTLITIGLPEPOTLFEIVFQLLNFFSGVFVSSLIQ 440
Db 477 GSTHWYDGVNSYIRCYFAVKTLITIGLDPDKTLFEIVFQLLNFFSGVFAFVMIQ 536
Qy 441 MRDVIKAATANQNYFRACMDDTIAYMNNYSIPKLVQKRVRTWYETWDSQRMDESDDLK 500
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Db 537 MRDVVGAATAGTYYRSCWDSTVKYMFYKIPKSVQNRVKTWYETWHSQGMDESELMV 596  
Qy 501 TLPTTVQALALADVNFSIISKVDLPKGDQMIYDMLRLKSLVLPKGFVCKKGEIGKE 560  
Db 597 QLPDKWRJLDLADVNINISVKVAFQGGCDQMFDMRLKRLSVVLPNDYVCKKGEIGRE 656  
Qy 561 MYIKHGEVQVLGGPDGKTVLTKAGSVFGEISLLAAGGNNRRTANVAHGFANLLFLD 620  
Db 657 MYIIQAGQVQLGGPDGKSLVTLKAGSVFGEISLLAAGGNNRRTANVAHGFANLLFLD 716  
Qy 621 KKTLOEILVHVPDSERILMKARVLKOKAKTAETATPPKDLALLFPKKEETPKLFTLL 680  
Db 717 KCDLNEILVHYPESQKLKARRMLRSNNK-----PKEEKSVLILPPRAGTPKLFNAAL 771  
Qy 681 GGTGKAS-----LARLLKREQAOKKENSEGEGEKENEDKQK 728  
Db 772 AMTGKGGKAGKGLAHLRLARLLELALEAAKHEEL---VEQAKSQDVKGEGSAAP 828  
Qy 729 ENEDKGE-NEDKOKGREPEKPLDRPECTASPIAV-----EEBPHSVRRTVLP 776  
Db 829 DQHTHPKEATDPPAPRTPEPP-GSPSPSPASLGSGEGEGEPAPPEHSVR-----882  
Qy 777 RGTSRQSLIISMAPSAGGEBVLITVEKKAQ 809  
Db 883 -----ICMSGPEPEGEILSVKMPERE 906

## RESULT 4

US-09-949-016-10215  
; Sequence 10215, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10215  
; LENGTH: 698  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-10215

Query Match 20.2%; Score 857; DB 4; Length 698;  
Best Local Similarity 29.9%; Pred. No. 2.6e-67;  
Matches 226; Conservative 153; Mismatches 272; Indels 106; Gaps 22;

Qy 19 NEQSSRNESGSHPSNQSQTQAQENKGBEKSILKTSPTVTSSEPHNTIQDKLSKNS 78  
Db 1 QTEKMAKINTQYSHPS-----RTHLVK-----TSRDLNRAENGLSRAHS 41  
Qy 79 SGDLTTNPQNAAEPTGTVPQKEMDPKGNPSPQNKPPAAPVINEYADAQLHNLVLR 138  
Db 42 SSBETS-----SVLPQ-GIAMESTRGLADSGGSGFTGQ-----GIARLSRLIFL 83  
Qy 139 MRQRTALYKKLVBEGDLSSP-----EASPTAKFTAVPPVKESDDKPTHEYRLLM 189  
Db 84 LRRWAARVHHODQPDSPDFRFRGAELKEVSSQESNAQANVGSOEPADRG-----RSW 138  
Qy 190 FKVKMPL-----TEYLKRIKLPNSI-DSYTDRLYLILWLLVTLAYNNWCWFTPL 238  
Db 139 -----PLAKCNTNTSNNTBEEKTKKDAIVDPFSSNLYRRLTAIALPVPFYNWYLLIC 192

Qy 239 RLVPFYQTAADNIHYWLADIICDIYLYDMLFIQRIQFVRGGDIIVDSNELRKHRTST 298  
Db 193 RACFDELQSEYLMWLVLVDSADVLVLDL-VRARTGFLBQGLMVSDTNRLWQHYKTTT 251  
Qy 299 KFQLDVASIIPFDICYLFFGFEN-PMFRANRMLKTSPEFNNHLESIMDKAYIVRVT 357  
Db 252 QFKLDVLSLVPDLDLAIYLVKVTNYPEVFRNLLKFSRLEFFDRTETRTNYNPMFRIGNLV 311  
Qy 358 GYLFIHLHINACVYMASNVEGIGTTRWVYDG-----EGNEYLRCYYWAVRLLITIG 409  
Db 312 LYILIIHWNACIVFAISKFGTGDVSNVYNIPIPEHGRLSRKVIYLSLYSTLTLTIG 371  
Qy 410 GLPBPQTLFEIVFOLLNPFSGVFFVSSLIGQMRDVIQAATANQNYFRACMODDTIAYMNY 469  
Db 372 ETTPPVKDEEYLFVVDVFLVGLVFIATIVGVNGSMISNMNASRAEFQAKIDSIKQYMQFR 431  
Qy 470 SIPKLVQKVRVTVEYTWDSQRLMDESDLLKTLPTTVQLALADVNFVSIISKVDLPKGC 529  
Db 432 KVTIDLETRVIRWFYDLWANKVTYDEKEVLSLDPKLAETAINVHLDLTKKVRIFQDCE 491  
Qy 530 TQMIYDMLRLKSLVLPKGFVCKKGEIGKEMYIIKHGEVQVLGGPDGKTVLTKAGSV 589  
Db 492 AGLLVELVLKRPVFPSPGDYICKGDIGKEMYIINEGKLAVV-ADGVTQFVVLSDGSY 550  
Qy 590 FGEISLLAAGG---GNRRTANVAHGFANLLTLDKKTLQELIVHYPDSERILMKAR-VL 645  
Db 551 FGEISILNKGSGNNRTANIRSIGYSDLPCLSKODLMEALTEYPEAKKALEEKGQIL 610  
Qy 646 LKQK---AKTAETPPPKDLALLPPKEETPKLFTLLGGTGKASLARLL-----KL 694  
Db 611 MKONLIDELARAGADPKDL-----BEKVEQLGSSL--DTLQTRFARLLAEYNATQMKM 662  
Qy 695 KREQAOKKENSEGEE---EGKENEDKQKENEKQK 728  
Db 663 KQRLSLESQVKGSGDPLADGEVPGDATK-TEDKQK 698

## RESULT 5

US-09-538-092-1351  
; Sequence 1351, Application US/09538092  
; Patent No. 6753314  
; GENERAL INFORMATION:  
; APPLICANT: Giot, Loic  
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
; FILE REFERENCE: 15966-542  
; CURRENT APPLICATION NUMBER: US/09/538,092  
; CURRENT FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/127,352  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/178,965  
; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 1387  
; SOFTWARE: CuratSeqformatter Version 0.9  
; SEQ ID NO 1351  
; LENGTH: 694  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Polypeptide Accession Number Q16281  
US-09-538-092-1351

Query Match 20.1%; Score 850; DB 4; Length 694;  
Best Local Similarity 30.0%; Pred. No. 1.1e-66;  
Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

Qy 27 NEEGSHPSNQSQTQAQENKGBEKSILKTSPTVTSSEPHNTIQDKLSKNSGDLTNP 86  
Db 5 NTQYSHES-----RTHLVK-----TSRDLNRAENGLSRAHSSEETS-- 43  
Qy 87 DPQNAABPTGTVPKQKEMDPKGNPSPQNKPPAAPVINEYADAQLHNLVLRMRQRTALY 146





; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 1387  
; SOFTWARE: CurapatSeqformatter Version 0.9  
; SEQ ID NO 1037  
; LENGTH: 686  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (10)..(6)  
; OTHER INFORMATION: Polypeptide Accession Number P29973  
US-09-538-092-1037

Query Match 19.3%; Score 817; DB 4; Length 686;  
Best Local Similarity 29.9%; Pred. No. 9.2e-64;  
Matches 226; Conservative 129; Mismatches 266; Indels 136; Gaps 24;

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QY 5 LTKNVKVPICGENNENEGSSRRNEEGSHPS-----NQSOQTAAQENKGE-----KSL 53
DB 13 VTMPNVIVP-----DIEKEIRRMENGACSSFSEDDSDASTSESEENPHARGSFYSKSL 67
QY 54 KTKSTPTVTSSEPHNTIQDKLSKNSGDLTTPDQNAAEPTGTVPQEKMDPGKGPNS 113
DB 68 R-KGSPSQREQLPGALFNVNNS-----NKD-----QEPEKKKKKKKSKSDDKNE 117
QY 114 POKPPAAPVINEYADAQLHNLVKRMQRTALYKKGVLVEGDLSSPEASPTAKPTAVPPV 173
DB 118 NKNDPE-----KKKKKKKKKK-----E 137
QY 174 KESDDKTEHYRLLWFKVKKMPLETKRIKLPNSIDSYDRLYLMLLVTL--AYNW 231
DB 138 ESKDKKEE-----KKEVV-----IDP-SGNTYNNWLCITLIPVMYNW 176
QY 232 NCWFPIRLVFPYQADNIHYWLIADIIICDIYLYDMLFIQPLQFVRGGDIIVDSNELR 291
DB 177 T--WVIARACFDELQSDVLEWLLDYVSDIVLIDM-FVTRTGYLEQGLLVKEELKLI 233
QY 292 KHYRTSTKFDLVASIIIPFDICYLFFGN-PMFRANRLKMTSPFEPNHLESIMDKAYI 350
DB 234 NKYSNLQFKLDVLSLITDLYLFGKGNVPEIRNLRLFRSMPFQRTETRTNYNI 293
QY 351 YRVIRTTGYLLFILHINACVYVWASNYEGIGTTRWVY-----DGE-----GNEYLRCYWAV 402
DB 294 FRISNLVWYVIIHWNACVYSISKAIGFNGDWTWVPDINDPEFGRILARKYVSLYWS 353
QY 403 RLTITIGLPEPQTLFEIVFOLLNFFSGVVFSSLIQOMRDVIGAAATANQYFRACMDDT 462
DB 354 LTLTIGETPPVRDSEVVFVDFLIGLVLFATIVGNIGSMISNMNARAFAEQRIDAI 413
QY 463 IAYMNNYSIPKLQKRVRTWYEYTWDSQRMDESDLLKTLPTTQLALADIVNFSISKV 522
DB 414 KQYMHFRNVSKDMKRVIKWFDYLTWTKTDEKEVLKLPDKLRAEIAINVHLDLTKV 473
QY 523 DLFGCDTQMYDMLRLKSVLYLPDGFVCKKGIGKEMWYIIKHGEVQVLGGPQTKVLV 582
DB 474 RIFADCEAGLLVELVLKLPQVYSPGDIYCKKGIGREMYIIKEGKLVV-ADGVTOFV 532
QY 583 TLKAGSVFGEISLLAAGS---GNRRTANVVAHGFANLLTLDKKTLOEILVHYPPSERILM 639
DB 533 VLSGYSYFGEISILNIGSKAGNRRTANIKSIGYSDLFCLSKDDLMALTEYPPDAKTMLE 592
QY 640 KQARVLLKQKA-----KTAETATPPRKLALLPPKKEETPKLTKLGGTGKASLARLL--- 692
DB 593 EKGQILMKDGLLDLNIANAGSDPKOLEEKVTRMEGSDVLLQT-----RFAILAEY 644
QY 693 -----KLKREAAOKK-----ENSEG-GBEEG 713
DB 645 ESMQOKLQRLTKVEKFLKPLIDTEFSSIEGPGAESG 681
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RESULT 8  
US-09-949-016-11549  
; Sequence 11549, Application US/09949016

; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11549  
; LENGTH: 694  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-11549

Query Match 19.3%; Score 817; DB 4; Length 694;  
Best Local Similarity 29.9%; Pred. No. 9.4e-64;  
Matches 226; Conservative 129; Mismatches 266; Indels 136; Gaps 24;

```
QY 5 LTKNVKVPICGENNENEGSSRRNEEGSHPS-----NQSOQTAAQENKGE-----KSL 53
DB 21 VTMPNVIVP-----DIEKEIRRMENGACSSFSEDDSDASTSESEENPHARGSFYSKSL 75
QY 54 KTKSTPTVTSSEPHNTIQDKLSKNSGDLTTPDQNAAEPTGTVPQEKMDPGKGPNS 113
DB 76 R-KGSPSQREQLPGALFNVNNS-----NKD-----QEPEKKKKKKKSKSDDKNE 125
QY 114 POKPPAAPVINEYADAQLHNLVKRMQRTALYKKGVLVEGDLSSPEASPTAKPTAVPPV 173
DB 126 NKNDPE-----KKKKKKKKKK-----E 145
QY 174 KESDDKTEHYRLLWFKVKKMPLETKRIKLPNSIDSYDRLYLMLLVTL--AYNW 231
DB 146 ESKDKKEE-----KKEVV-----IDP-SGNTYNNWLCITLIPVMYNW 184
QY 232 NCWFPIRLVFPYQADNIHYWLIADIIICDIYLYDMLFIQPLQFVRGGDIIVDSNELR 291
DB 185 T--WVIARACFDELQSDVLEWLLDYVSDIVLIDM-FVTRTGYLEQGLLVKEELKLI 241
QY 292 KHYRTSTKFDLVASIIIPFDICYLFFGN-PMFRANRLKMTSPFEPNHLESIMDKAYI 350
DB 242 NKYSNLQFKLDVLSLITDLYLFGKGNVPEIRNLRLFRSMPFQRTETRTNYNI 301
QY 351 YRVIRTTGYLLFILHINACVYVWASNYEGIGTTRWVY-----DGE-----GNEYLRCYWAV 402
DB 302 FRISNLVWYVIIHWNACVYSISKAIGFNGDWTWVPDINDPEFGRILARKYVSLYWS 361
QY 403 RLTITIGLPEPQTLFEIVFOLLNFFSGVVFSSLIQOMRDVIGAAATANQYFRACMDDT 462
DB 362 LTLTIGETPPVRDSEVVFVDFLIGLVLFATIVGNIGSMISNMNARAFAEQRIDAI 421
QY 463 IAYMNNYSIPKLQKRVRTWYEYTWDSQRMDESDLLKTLPTTQLALADIVNFSISKV 522
DB 422 KQYMHFRNVSKDMKRVIKWFDYLTWTKTDEKEVLKLPDKLRAEIAINVHLDLTKV 481
QY 523 DLFGCDTQMYDMLRLKSVLYLPDGFVCKKGIGKEMWYIIKHGEVQVLGGPQTKVLV 582
DB 482 RIFADCEAGLLVELVLKLPQVYSPGDIYCKKGIGREMYIIKEGKLVV-ADGVTOFV 540
QY 583 TLKAGSVFGEISLLAAGS---GNRRTANVVAHGFANLLTLDKKTLOEILVHYPPSERILM 639
DB 541 VLSGYSYFGEISILNIGSKAGNRRTANIKSIGYSDLFCLSKDDLMALTEYPPDAKTMLE 600
QY 640 KQARVLLKQKA-----KTAETATPPRKLALLPPKKEETPKLTKLGGTGKASLARLL--- 692
DB 601 EKGQILMKDGLLDLNIANAGSDPKOLEEKVTRMEGSDVLLQT-----RFAILAEY 652
```

```

; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-46624

Query Match          9.8%; Score 416.5; DB 4; Length 256;
Best Local Similarity 36.8%; Pred. No. 9.6e-29;
Matches 78; Conservative 53; Mismatches 80; Indels 1; Gaps 1;

Qy 253 WLADIICDIYLDMLFIQPRQLQFVRGGDIIVDSNELRKHYRTSTKTKOLDVASIIPDI 312
Db 45 WLACDFCADIYLLDVVFKHRVMYLFEGFWKKNLTKKNYMRKLQPKLIDLALLPLEL 104

Qy 313 CYLFFGPNMF-RANRMLKYTSFFRNHLSIMDKXIVYRITTYGLFTLHINACVY 371
Db 105 LYPKLGTAQWLRFPFRFKIQSFWEVFRLLDRVISSPHVRVAKILTWMYMIHTAALY 164

Qy 372 YMASNYEGIGTRWVYDGEENEYLCYYWAVRTLITIGSLPBPQTLFEIVFOLLNFFSGV 431
Db 165 YAYSDDYQGLGNRWVFSKGHPVRCFAFATKTATSIGKNPKPQEQGYETVMTVAWLMGV 224

Qy 432 FVFSLLIGQMRDVIGATATQNYFRACMDTI 463
Db 225 FVFALLIGQIRDIISTATRNKHEYQLEDETL 256

RESULT 11
US-09-949-016-6615
; Sequence 6615, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6615
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6615

Query Match          9.8%; Score 413; DB 4; Length 1203;
Best Local Similarity 23.9%; Pred. No. 2.2e-27;
Matches 152; Conservative 109; Mismatches 273; Indels 101; Gaps 25;

Qy 62 SERPHTNIQKLSKKN--SSGDLTTNPD---PQNAAEPTGTVPQKEMDPGKE-----GP 111
Db 115 SGSSHGHLDHSAEERLLIAGDASPGEDRTTPGLAAEPE-----RPGASAQPAASP 165

Qy 112 NSPQNKPPAAPVINEYADALHNLVKRMRQRTAL-YKKKLVEGDSSPSPASQPTAKPTAV 170
Db 166 PPGQPPQPPASACEQPSVD-----TAIKVEGGAAGADQTLPEAEVRLGQAGFM 214

Qy 171 PPVKESDDKPEHYHYRLLMFKVKKMPLEVLKELPN--SIDSYTD-RLYLLWLLLVTL 227
Db 215 QROFGAMLQGVNKFSLRMFGSQKAVEREQ-ERKKSAGFWIHPYSDFRFY--WDLTMLL 271

Qy 228 AYNNWCWFIFLRVLPVFPYQTADNIHYWLIADIIICDIYLDMLFIQPRQLQFVRG-----G 281
Db 272 LMVGNLIIIPVGITF--FKDENTTPWVENVSDTFFLIDLV-----LNFRTGIVVEDNT 324

Qy 282 DIIVDSNELRKHYRTSTKTKOLDVASIIPDICYL-----PFGNPMF 323
Db 282 DIIVDSNELRKHYRTSTKTKOLDVASIIPDICYL-----PFGNPMF 323

; ORGANISM: Homo sapiens
US-09-275-252A-18

Query Match          11.4%; Score 484; DB 4; Length 261;
Best Local Similarity 37.2%; Pred. No. 9.6e-35;
Matches 97; Conservative 58; Mismatches 94; Indels 12; Gaps 4;

Qy 370 VYWASNYEGIGTRWVY----DGE-----GNEYLRCYYWAVRTLITIGSLPBPQTLFEIV 421
Db 1 IYVAISKSIGFVDYTWVYNNITDPEXYGLAREVIYCLYWSTLTITIGETPPPVKDESVL 60

Qy 422 FOLLNFFSGVVFSSLIGQMRDVIGATATQNYFRACMDTTAYNNVYSIPKLQKRVRT 481
Db 61 FVIFDFLIGLIVFATIVGNVGMISNNATRAEFQAKIDAVKHYMQFRKVSQKMEAKVIR 120

Qy 482 WYETWDSQRMDESLLKTLPTVOLALADVNPESIIISKVDLEFKGCDTOMLYDMLRLK 541
Db 121 WFDYLTNKTIVDEREILKMLPAKRAETAINVHLSTLKKVRFHDCAGLLVVELKLRL 180

Qy 542 SVLYLPDGFVCKKGEIGKEMYYIIKHGEVQVLGGPDGTVLTKAGSVGEISLAAAG- 600
Db 181 PQVFSFGDYICRKGDIGKEMYYIIKEGLAVV-ADDGVTQVALLSAGSCFGEISILNKG 239

Qy 601 --GNRTANVAVGFANLLTL 619
Db 240 KMGNNRTANIRSLGYSDLFCL 260

RESULT 10
US-09-270-767-46624
; Sequence 46624, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46624
; LENGTH: 256
; TYPE: PRT

```

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Db 325 EILDPQRIKMYLKSWMVDFTISSIPVDYIFLIVETRIDSEVYKTBARALIVRFTKIL 383
Qy 324 RANRLKYTSFFFNHLESIMDKAY-----IYRVIRTTGYLLFLFILHINACYVWASNYE 378
Db 384 SLRLRLRLIRYIHOWEEIFHMYDILASAVRIVNLIGMMLLCHWDGCLQFLVPLMLQ 443
Qy 379 GIGTRW-----VVDGEGNEYLRYCYYWAVRLTIG-GLPEPQTLFEIVFOLLNFFPSGV 431
Db 444 DFPDCCWYSINNMVNNSSGQYSVALFRAMSHMLCIGYGROAPVGMGSDVWLTMLSMIVGA 503
Qy 432 FVFSLLIGMRDVIIGAATANQYPRACMDDTIAYNNYSIPKLQKRVRTWVEYTWDSQR 491
Db 504 TCYAMFICHATALQSLDSSRRQYQYKQVEQYMSFHLGPPDRQRIDHYEHRYQG-K 562
Qy 492 MLDSDLLKTLPTTVQLALADVNFS-----IISKVDLFGCDTQMIYDMLLRKLSVLYLPG 548
Db 563 MFDEESILGELSEPLREEI---INFNCRKLVASMPLFANADPNFVTSMLTKLRPEVFPQG 619
Qy 549 DFCVCKGIGKEMYIIKHGEVOVL-GGPDGTQVLVTLKAGSVFGEISLLAAGGNRRATAN 607
Db 620 DYIIREGTIGKMYFIQHGVSVLTKGNKETK---LADGSYFGEICILLTRG---RRTAS 672
Qy 608 VVAHGFANLLTKDKTLQELIIVHYVPDSEIRILMKKA 642
Db 673 VRADYCRKLSLSDNFDNFEVLEEYP-----MMRRA 702
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## RESULT 12

```
US-08-997-685A-2
; Sequence 2, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997.685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
```

LENGTH: 910

TYPE: PRT

ORGANISM: mouse

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (130)..(148)

OTHER INFORMATION: S1

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (164)..(185)

OTHER INFORMATION: S2

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (208)..(229)

OTHER INFORMATION: S3

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (243)..(271)

OTHER INFORMATION: S4

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (291)..(313)

OTHER INFORMATION: S5

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (332)..(358)

OTHER INFORMATION: P

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (367)..(387)

OTHER INFORMATION: S6

FEATURE:

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; NAME/KEY: DOMAIN
; LOCATION: (472)..(602)
; OTHER INFORMATION: CNB
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AAC53518
; DATABASE ENTRY DATE: 1997-12-27
; RELEVANT RESIDUES: (1)..(910)
US-08-997-685A-2
```

## Query Match

9.7%; Score 412.5; DB 4; Length 910;

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Best Local Similarity 20.2%; Pred. No. 1.6e-27;
Matches 150; Conservative 144; Mismatches 269; Indels 179; Gaps 25;
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Qy 210 IDSYTD-RLYLLMLLLVTLAYNNWCWFIPLRLVFPYQYADNIHMYLADIICDIYLYDM 268
Db 124 IHPYSDFRFY--WDLIMLMVGNLVIIPVGITE--FTEQTTTPWIFNVASDTVFLDL 179
Qy 269 LPIQPRLOFVRG-----GDIIIVDSNELRKHRYSTKFDLDVASIIPDICYL----- 315
Db 180 I-----MNFRTGTVNESSEIILDPKVIKMYLKSWM-FVVDFTISSIPVDYIFLIVEKGM 233
Qy 316 -----FFGFNPMFRANRLKVTSPFEFNHLESIMDKAY-----IYRVIRTTGY 359
Db 234 SEVYKTBARALIVRFTKILSLRLRLRLRLIRYIHOWEEIFHMYDILASAVRIFNLIGM 293
Qy 360 LLFILHINACYVY-----WASNYEGIGTRTWVYDGEENEYLRVCYVAVRITLT 407
Db 294 MLLCHWDGCLQFLVPLLDQPPDCWVSLNE-----WVNDSWGKQYSYALFKAMSHMLC 347
Qy 408 IG-GLPEPQTLFEIVFOLLNFFSGVVFSSLIQMRDVGATATANQYPRACMDDTIAYM 466
Db 348 IGYGAQAPVSSDLWITMLSMIVGATCYAMFVGATATLIQSLDSSRRQYQYKQVEQYM 407
Qy 467 NNYSIPLKLVQKRVRTWVEYTWDSORMLDESLLKTLPTTVQLALADVNFS-----IISKVD 523
Db 408 SFHLKPADMRQKHIDHYEHRYQG-KIFDEENILSELNDPLREEI---VNFNCRKLAVATMP 463
Qy 524 LFGCDTQMIYDMLLRKLSVLYLPGDFVCKKGIGKEMYIIKHGEVOVLGPDGTQVLVLT 583
Db 464 LFNADPNFVTAMLSKLRFVFPQDVIIREGAVGKMYFIQHGVAAGVI-----TKSSKE 518
Qy 584 LKA--GSVFGEISLLAAGGNRRATANVVAHGFANLLTKDKTLQELIIVHYVPDSEIR 636
Db 519 MKLTDGSYFGEICILLTRG---RRTASVRADYCRKLSLSDNFDNFEVLEEYPMRRAPETV 575
Qy 637 -----ILMEK-----ARVLLKQKAK----- 651
Db 576 AIDRLDRIGKNSILQKQKDLNTGVNNGEENILKQIVKHDREMQAIPPIYQMTA 635
Qy 652 ---TAEATPPRKOL-----ALLFP-----P 668
Db 636 LNCITSSITTPISRMRQTQSPVYTATSLSHSNLHSPSPSTQTPQPSAILSPCSYTTAVCSP 695
Qy 669 KBETPKLFTLLGGTGKASLARLLKLKREQAQ---KKENSEGEGEEKENEDKOKENED 725
Db 696 PIQSPLATRTFHVASPTASQLSLMQPQQQLPQSQVQQTQTQTQQQQQQQQQQQQQQQQ 755
Qy 726 KOKENEDKGENEDKDKGREPEEKPLDRPCECTASPIAVEEPEHPHVRRTVLRGTTSRSL- 784
Db 756 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQPQTPGSGTSPKNEVHKSTOALHNTLTKTEVRLSASQPSLP 815
Qy 785 -----IISMAPSAEGGEEVLTI 801
Db 816 HEVSTLIS-RPHPTVGSLSASI 836
```

## RESULT 13

```
US-09-086-436-31
; Sequence 31, Application US/09086436
; Patent No. 6703485
; GENERAL INFORMATION:
; APPLICANT: Kandel, Eric R.
; APPLICANT: Santoro, Bina
```



## RESULT 15

US-09-949-016-6036  
; Sequence 6036, Application US/09949016

TELEPHONE NO. 0012333  
; GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

**TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF**

FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

**PRIOR FILING DATE:** 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237.768

PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 6036

LENGTH: 889

TYPE: PRT

ORGANISM: Human

US-09-949-016-6036

Query Match	9.68;	Score	405.5;	DB	4;	Length	889;												
Best Local Similarity	23.08;	Pred.	No. 6.4e-27;																
Matches	170;	Conservative	116;	Mismatches	301;	Indels	151;												
Gaps	29;																		
QY	83	TTNPDPQNAAEPTGTVP	EQK----	EMDPGEKGNPSPONKPP	AAPVINEYADAQLNLV	136													
DB	19	TTTGPPPPPPRP	-----	PKQPPPPPPPPAP	PPGPGAPQHPRAALP	PPAADP	CGPR 72												
QY	137	KWRQRTALYKKLV	EGDLSP	SPASQ----	TAKPTAVP	-----	171												
DB	73	GLRLSRDSSCGRP	CTGATAGS	PNGECGRGEPQCS	PAGPEGPARGPKVSP	SCRGAAS	132												
QY	172	-----	PVKESD	-----	-----	-----	195												
DB	133	GPAPGPGAPBAE	AGSEEA	GPAGEPRGSOAS	PMQRQFGALQPGV	NKFSLRMFGS	KAVERE 192												
QY	200	YLAKIKLPNS-	-IDS	YTD-RLYL	LWLLVTLAYNN	CWFPLRLVF-	-PYQTADNIHWL 254												
DB	193	Q-ERVS	SAGAWI	THPYS	DRPY--	WDFTMLLFMVGN	LIIPVGITPFKDETTAP----WI 245												
QY	255	IADI	CDI	IYLV	DMLFTQ	PLQ	LVRG-----GDII	VDSNELKHYRTSTK	FQLDVASII 308										
DB	246	VFNW	SDTF	FLMD	LV-----	LNFR	TGIVIEDNTE	BIILDPEKIKKY-LRTW	FVVDVFSII 299										
QY	309	PF	DICV	L-----	-----	PGFN	PMFRANRMLKY	TSEFFFNHLESIM	KAY- 349										
DB	300	PVDY	I	FLIVE	KEGID	SEVYK	TARALIRV	FRFTKILSLRL	SLRIYIHOWEEIFHMYD 359										
QY	350	-----	IYRV	IRTGTGYLL	FILHINAC	YVWASNYEG	IGTTRWV-YDGE	NE-----	YLRCYV 399										
DB	360	LASAV	MRI	CNLI	SMWLL	CHWD	GCLQ	FLVPM	LQDFPRNCWVSINGMWNH	SWSELYSALP 419									
QY	400	WAVR	TLIT	IG-GU	PEPOTL	FEIV	QLN	FFSGV	VFSSLI	QOMRDVIGA	TANQNYFRAC 458								
DB	420	KAMSH	MLCIGYGR	QAPES	MTD	IWL	TMSLV	MGATCYAM	FICHATALLI	QSLDSSRRQYOEK 479									
QY	459	MDDTI	AMNYS	TPKL	VOKVR	TYEY	TWDS	QRM	DES	LLKTLPTTV	QLALADVNFSP- 517								
DB	480	YKQVE	QYSPH	KLPA	DPRQ	KIHDI	YEHRYQ	Q-KMF	DESD	SLGELNG	FLREI---VNFNC 535								
QY	518	--	IISK	VDLP	FKG	CDTQ	MIYDML	RLKSV	LYLP	GD	FVCKGEIGKEM	YIIKHGEVOVLGGP 575							
DB	536	RKL	VAS	MP	L	FANAD	PNFV	TANIL	TKL	KEV	QPGDYI	IREGTI	GKNFYI	QHGVSUJ--T 593					
QY	576	DGT	KVL	VT	L	KAGS	VFGE	IS	ILAA	AGGN	RNR	TANV	VV	AHGF	ANL	LLTLDK	KTQL	OEILLV	HYPDSE 635

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 27, 2005, 18:01:32 ; Search time 129 Seconds  
(without alignments)  
2425.497 Million cell updates/sec

Title: US-09-855-828-1  
Perfect score: 4234  
Sequence: 1 MFKSLTKVKNVKPIGENNEN.....PSAEGGSEVLTIYEKAKQ 809

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4234	100.0	809	5	AAE15982 Human cyc
2	4231	99.9	809	5	AAE15983 Human CNG
3	4231	99.9	809	5	AAE15985 Human CNG
4	4229	99.9	809	5	AAE15984 Human CNG
5	4228	99.9	809	5	AAE15986 Human CNG
6	1948.5	46.0	1250	8	ABM83979 Human dia
7	1781.5	42.1	652	4	ABG27471 Novel hum
8	1103	26.1	1037	4	ABG66545 Drosophil
9	1088	25.7	644	4	ABG05466 Novel hum
10	955	22.6	747	4	ABG11969 Novel hum
11	906	21.4	237	6	ABR33396 Amino aci
12	902	21.3	237	6	ABP98584 Amino aci
13	850	20.1	694	5	AAE15987 Human CNG
14	850	20.1	694	7	AAE38591 Human CNG
15	831.5	19.6	683	7	ADD48638 Rat Prote
16	829	19.6	663	5	AAE15982 Cow HBMYC
17	829	19.6	663	6	ABG74912 Bovine CN
18	826.5	19.5	698	8	ADQ67650 Novel hum
19	825.5	19.5	664	5	AAE15987 Variant H
20	824	19.5	663	6	ABG74914 Bovine CN
21	823	19.4	663	6	ABG74913 Bovine CN
22	821.5	19.4	664	6	ABG72530 Novel hum
23	820.5	19.4	664	5	AAE15987 HBMYCNG
24	820	19.4	732	5	AAE15987 Rabbit HB
25	819.5	19.4	664	4	AAE04894 Human tra

26	819.5	19.4	664	5	ABB78066 Amino aci
27	819.5	19.4	664	6	ABG72529 Novel hum
28	819.5	19.4	664	6	ABU12049 Human NOV
29	819.5	19.4	664	6	ABP98475 Amino aci
30	818.5	19.3	690	7	ADD93244 Cyclic nu
31	818.5	19.3	690	8	ADI38341 Human pro
32	817	19.3	686	7	ADD48640 Human pro
33	816.5	19.3	664	8	ADR09903 Human pro
34	815	19.2	690	5	AAE15988 Human CNG
35	804	19.0	664	5	AAE15988 Human CNG
36	804	19.0	664	5	AAE15988 Human CNG
37	804	19.0	664	6	AAE37219 Rat CNG c
38	804	19.0	664	7	ADF56504 Rat CNG c
39	795	18.8	664	7	ADF56501 Modified
40	791	18.7	664	6	AAE37220 Rat CNG c
41	791	18.7	664	7	ADF56502 Modified
42	790	18.7	664	6	AAE37224 Rat CNG c
43	790	18.7	664	6	AAE37223 Rat CNG c
44	782	18.5	664	6	AAE37222 Rat CNG c
45	777.5	18.4	664	5	AAE15982 Mouse HBM

ALIGNMENTS

RESULT 1	
AAE15982	AAE15982 standard; protein; 809 AA.
XX	AAE15982
AC	AAE15982;
XX	XX
DT	26-MAR-2002 (first entry)
XX	XX
DE	Human cyclic nucleotide-gated cation channel 3 beta subunit protein.
XX	XX
KW	Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;
KW	cyclic nucleotide-gated ion channel; contraceptive; vision disorder;
KW	male infertility; genetic defect; reporter-ligand interaction; CNG;
KW	viral infection; cancer.
XX	XX
OS	Homo sapiens.
XX	XX
FH	Key Location/Qualifiers
FT	Region 210..661
FT	/note= "Conserved region; this region also function as an
FT	epitope and is referred in claim 1"
XX	XX
FN	WO200188090-A2.
XX	XX
PD	22-NOV-2001.
XX	XX
PF	15-MAY-2001; 2001WO-US015814.
XX	XX
PR	15-MAY-2000; 2000US-0204445P.
PR	14-MAY-2001; 2001US-00855828.
XX	XX
PA	(ICAG-) ICAGEN INC.
XX	XX
PI	Crech CD, Jegla TJ;
XX	XX
DR	WPI; 2002-089847/12.
DR	N-PSDE; AAD25729.
XX	XX
PT	New polypeptide, useful for screening for modulators of cyclic nucleotide
PT	-gated ion channels, comprises the isolated cyclic nucleotide-gated
XX	XX
PS	cation channel 3 beta subunit.
XX	XX
CC	Claim 12; Fig 4; 83pp; English.
XX	XX
CC	The invention relates to human cyclic nucleotide-gated cation channel 3
CC	beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member
CC	of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms
CC	functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha

CC subunits that are expressed in retina. CNG3B polypeptides are useful for  
CC screening modulators of CNGs which are useful as contraceptives and for  
CC treating various disorders involving cation channels, e.g. vision  
CC disorders and male infertility. Polynucleotides of the invention are  
CC useful for transfection of cells in vitro and in vivo, to correct  
CC acquired and inherited genetic defects, cancer and viral infections.  
CC Sequences of the invention are useful as reporter molecules in assays and  
CC detection systems, to measure changes in cation concentration, membrane  
CC potential, current flow, ion flux, transcription, signal transduction,  
CC reporter-ligand interactions and second messenger concentrations, in  
CC vitro, in vivo and ex vivo. They are useful to construct models of CNGs  
CC in a computer system and for examining expression and regulation of  
CC cation channels. The present sequence is human CNG3B protein

Sequence 809 AA:

```
Query Match      100.0%; Score 4234; DB 5; Length 809;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1	MFKSLTKVNKYKPTGENNENECSSRRNEEGSHPSNOSQOTTAOENKGEKSLTKTKSPV	60
Db	1	MFKSLTKVNKYKPTGENNENECSSRRNEEGSHPSNOSQOTTAOENKGEKSLTKTKSPV	60
Qy	61	TSEBPHNTNIQDKLSKKNSSGDLTTNPDQONAAEPTGTVPQEKEMDPGKEGPNSPQNKPPA	120
Db	61	TSEBPHNTNIQDKLSKKNSSGDLTTNPDQONAAEPTGTVPQEKEMDPGKEGPNSPQNKPPA	120
Qy	121	APVINEYADAQHLNLVKRMRQRTALYKKKLVEGDLSSPEASQOTAKPTAVPPVKESDDKP	180
Db	121	APVINEYADAQHLNLVKRMRQRTALYKKKLVEGDLSSPEASQOTAKPTAVPPVKESDDKP	180
Qy	181	TEHYRLLFWFKVKQKMPLEYLKRKLPSIDISYTDRLYLLMLLLTTLAANNWCWFIPLRL	240
Db	181	TEHYRLLFWFKVKQKMPLEYLKRKLPSIDISYTDRLYLLMLLLTTLAANNWCWFIPLRL	240
Qy	241	VFPYQTADNIHWLIADIICDIIYLYDMLFIQPRLQFVRGGDIIIVDSNELRKHXYTSTKF	300
Db	241	VFPYQTADNIHWLIADIICDIIYLYDMLFIQPRLQFVRGGDIIIVDSNELRKHXYTSTKF	300
Qy	301	QLDVASIIIPDICYLFFGFPNMFANRMLKYTSPFEFNHLESIMDKAYIYRVIRTGYL	360
Db	301	QLDVASIIIPDICYLFFGFPNMFANRMLKYTSPFEFNHLESIMDKAYIYRVIRTGYL	360
Qy	361	LFILHINACVYWNASNYEGIGTRWVYDGBGNEYLRCCYVWVRTLITIGGLEPEPOTLFEI	420
Db	361	LFILHINACVYWNASNYEGIGTRWVYDGBGNEYLRCCYVWVRTLITIGGLEPEPOTLFEI	420
Qy	421	VFOLLNPFSGVVFVSSLIGQMRDVTGAATANQNYFRACMDDTIAYMNNYSIIPKLQKQYR	480
Db	421	VFOLLNPFSGVVFVSSLIGQMRDVTGAATANQNYFRACMDDTIAYMNNYSIIPKLQKQYR	480
Qy	481	TWYEYTWDSQRMLEDSDLLKTLPTTVQLALADIVNFSIISKVDLPKGCOTQMIYDMLLRL	540
Db	481	TWYEYTWDSQRMLEDSDLLKTLPTTVQLALADIVNFSIISKVDLPKGCOTQMIYDMLLRL	540
Qy	541	KSVLYLPGDFVCKGGEIGKEMWIIKHGEVOVLGGPDGTVLTLTKAGSVFGEISLLAAGG	600
Db	541	KSVLYLPGDFVCKGGEIGKEMWIIKHGEVOVLGGPDGTVLTLTKAGSVFGEISLLAAGG	600
Qy	601	GNRRTANVAHGAFANLLTLDKKTQLOEILVHYPDSEIRILMKKARVLLKQAKTAEATPPRK	660
Db	601	GNRRTANVAHGAFANLLTLDKKTQLOEILVHYPDSEIRILMKKARVLLKQAKTAEATPPRK	660
Qy	661	DLALLFPKKEETPKLFTLLGGTGKASLARLLKLKREQAAQKKNESGEGEEGKENEDKQ	720
Db	661	DLALLFPKKEETPKLFTLLGGTGKASLARLLKLKREQAAQKKNESGEGEEGKENEDKQ	720
Qy	721	KENEDQKENEDQKENEDKDGRBPEEKPLDRPECTASPIAVEEPHPSVRRTVLPRGHS	780
Db	721	KENEDQKENEDQKENEDKDGRBPEEKPLDRPECTASPIAVEEPHPSVRRTVLPRGHS	780
Qy	781	ROSLIISMAPSAEGGEEVLTIETVEKQAKQ	809

db 781 ROSLIISMAPSAEGGEEVLTIEVKEKAKO 809

## RESULT 2

AAE15983

ID AAE15983 standard; protein; 809 AA.

AC AAE15983;

26-MAR-2002 (first entry)

Human CNG3B protein variant #1 (R142K):

Human: cyclic nucleotide-gated cation c

KW cyclic nucleotide-gated ion channel; vision disorder  
KW male infertility; genetic defect; reporter-ligand interaction; CNG;  
KW viral infection; cancer; mutant; mutein; variant.  
KW cyclic nucleotide-gated ion channel; contraceptive; vision disorder

WV Homo sapiens

OS Homo sapiens  
OS Synthetic

XX	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
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63	63	63
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70	70	70
71	71	71
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78	78	78
79	79	79
80	80	80
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87	87	87
88	88	88
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94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

FH	key	LOC
FT	Misc-difference	142

FT FT

XX  
PN  
W0200188090-A2XX  
DD 22-NOV-2001XX  
DE  
15 MAY-2001. 2001WQ-IIS015814

15 MAY 2000 - 2000HS-03041415B

PR 15-MAY-2000; 2000US-0204443F.  
 PR 14 MAY. 2001: 2001US-00855828  
 PR 14 MAY. 2001: 2001US-00855828

XX  
DA (TCAG-) TCAGEN TNCXX  
DI  
Crescent City  
Tagliata MT.XX  
BT  
000000007/19

XX New polypeptide, useful for screening for modulators of cyclic nucleotide  
PT  
PT gated ion channels, comprises the isolated cyclic nucleotide-gated  
PT  
PT cation channel  $\beta$  subunit.

XX  
PG  
Disclosure: Page: 83nn: English:

The invention relates to human cyclic nucleotide-gated cation channel 3 beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms functional heteromultimers with CNGAL and/or CNGA3, two CNG alpha subunits that are expressed in retina. CNG3B polypeptides are useful for screening modulators of CNGs which are useful as contraceptives and for treating various disorders involving cation channels, e.g. vision disorders and male infertility. Polynucleotides of the invention are useful for transfection of cells in vitro and in vivo, to correct acquired and inherited genetic defects, cancer and viral infections. Sequences of the invention are useful as reporter molecules in assays and detection systems, to measure changes in cation concentration, membrane potential, current flow, ion flux, transcription, signal transduction, reporter-ligand interactions and second messenger concentrations, in vitro, in vivo and ex vivo. They are useful to construct models of CNGs in a computer system and for examining expression and regulation of cation channels. The present sequence is human CNG3B protein variant (R142K). Note: This sequence is not shown in the specification, but is derived from the human wild type CNG3B protein (SEQ ID NO:1) shown in Fig 4 of the specification (AAE15982).

Sequence 809 AA:

Query Match	99.9%	Score 4231;	DB 5;	Length 809;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 808;	Conservative	1;	Mismatches	0;
Indels	0;			Gaps



Qy 1 MFKSLTKVNVKVPICGNNENEGSSRRNEEGSHPSNQSOQTAAQENKGEKSLTKSTPV 60  
Db 1 MFKSLTKVNVKVPICGNNENEGSSRRNEEGSHPSNQSOQTAAQENKGEKSLTKSTPV 60  
Qy 61 TSEEPHTNIQDKLSKNSGGDLTTPDPQNAAEPTGTVPQEKMDPGKEGSPNQKPPA 120  
Db 61 TSEEPHTNIQDKLSKNSGGDLTTPDPQNAAEPTGTVPQEKMDPGKEGSPNQKPPA 120  
Qy 121 APVINEYADAQLHNLVKRMQRORTALYKKKLVEGDLSSPEASPTAKTAVPPVKESDDKP 180  
Db 121 APVINEYADAQLHNLVKRMQRORTALYKKKLVEGDLSSPEASPTAKTAVPPVKESDDKP 180  
Qy 181 TEHYRLWLFVKVKMPLTEYLKRIKLPNSIDSYDRLYLMLLLVTLAYNWNCFIPLRL 240  
Db 181 TEHYRLWLFVKVKMPLTEYLKRIKLPNSIDSYDRLYLMLLLVTLAYNWNCFIPLRL 240  
Qy 241 VFPYQTADNIHYWLIADIICDIIYLYDMLFTQPLQFVRGGDIIVDSNELRKHRTSTKF 300  
Db 241 VFPYQTADNIHYWLIADIICDIIYLYDMLFTQPLQFVRGGDIIVDSNELRKHRTSTKF 300  
Qy 301 QLDVASIIPFDICVYLFQFNPMFRANRMLKVTSPPEFNHLESIMDKAYIVRVIRTTGYL 360  
Db 301 QLDVASIIPFDICVYLFQFNPMFRANRMLKVTSPPEFNHLESIMDKAYIVRVIRTTGYL 360  
Qy 361 LFIHINACVYVYASNYEGIGTRWYDGEYRCLYCYWVRLTITIGGLPEPQTLFEI 420  
Db 361 LFIHINACVYVYASNYEGIGTRWYDGEYRCLYCYWVRLTITIGGLPEPQTLFEI 420  
Qy 421 VFQLLNPFSGVYVFSLLIGQMRDVIGATANTQNTFRACMDDTIATMNNYSIPKLQKVR 480  
Db 421 VFQLLNPFSGVYVFSLLIGQMRDVIGATANTQNTFRACMDDTIATMNNYSIPKLQKVR 480  
Qy 481 TWYETWDSQRMLESDDLKLTPTTVOLALADVNFSIISKVDLPKGCOTQIYDMLLRL 540  
Db 481 TWYETWDSQRMLESDDLKLTPTTVOLALADVNFSIISKVDLPKGCOTQIYDMLLRL 540  
Qy 541 KSVLYLPGDFCKGKEIGKEMYYIKHGEVQVLGGPDGTVKLVTLKAGSVFGEISLLAAG 600  
Db 541 KSVLYLPGDFCKGKEIGKEMYYIKHGEVQVLGGPDGTVKLVTLKAGSVFGEISLLAAG 600  
Qy 601 GNRRTANVAVGFANLLTDKKTQELVHYVPSERILMKARVLLKQAKTAETPPRK 660  
Db 601 GNRRTANVAVGFANLLTDKKTQELVHYVPSERILMKARVLLKQAKTAETPPRK 660  
Qy 661 DLALLFPKPEPKPLFKTLIGGTGASLARIKLLKREQAOKKENSEGEGEKENEDKQ 720  
Db 661 DLALLFPKPEPKPLFKTLIGGTGASLARIKLLKREQAOKKENSEGEGEKENEDKQ 720  
Qy 721 KENEDKQKENEKEDKDKGREPEKPLDRPECTASPIAVBEEPHSVRRTVLPRTS 780  
Db 721 KENEDKQKENEKEDKDKGREPEKPLDRPECTASPIAVBEEPHSVRRTVLPRTS 780  
Qy 781 RQSLIISMAPSAEGGEVLTIEVKEKAKQ 809  
Db 781 RQSLIISMAPSAEGGEVLTIEVKEKAKQ 809

RESULT 3

AAE15985 standard; protein; 809 AA.

AC AAE15985;

XX 26-MAR-2002 (first entry)

XX Human CNG3B protein variant #3 (L675V).

XX Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;  
XX cyclic nucleotide-gated ion channel; contraceptive; vision disorder;  
XX male infertility; genetic defect; reporter-ligand interaction; CNG;  
XX viral infection; cancer; mutant; mutein; variant.

OS Homo sapiens.  
XX Synthetic.

Key Location/Qualifiers

Misc-difference 675 /note= "Wild type Leu substituted with Val"

XX WO200108090-A2.

XX 22-NOV-2001.

XX 15-MAY-2001; 2001WO-US015814.

XX 15-MAY-2000; 2000US-0204445P.

XX 14-MAY-2001; 2001US-00855828.

XX (ICAG-) ICAGEN INC.

XX Creech CD, Jegla TJ;

XX WPI; 2002-089847/12.

XX New polypeptide, useful for screening for modulators of cyclic nucleotide-gated ion channels, comprises the isolated cyclic nucleotide-gated cation channel 3 beta subunit.

XX Disclosure; Page; 83pp; English.

XX The invention relates to human cyclic nucleotide-gated cation channel 3 beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha subunits that are expressed in retina. CNG3B polypeptides are useful for screening modulators of CNGs which are useful as contraceptives and for treating various disorders involving cation channels, e.g. vision disorders and male infertility. Polynucleotides of the invention are useful for transfection of cells in vitro and in vivo, to correct sequences of inherited genetic defects, cancer and viral infections. Sequences of the invention are useful as reporter molecules in assays and detection systems, to measure changes in cation concentration, membrane potential, current flow, ion flux, transcription, signal transduction, reporter-ligand interactions and second messenger concentrations, in vitro, in vivo and ex vivo. They are useful to construct models of CNGs in a computer system and for examining expression and regulation of cation channels. The present sequence is human CNG3B protein variant (L675V). Note: This sequence is not shown in the specification, but is derived from the human wild type CNG3B protein (SEQ ID NO:1) shown in Fig 4 of the specification (AAE15982)

XX Sequence 809 AA;

Query Match 99.9%; Score 4231; DB 5; Length 809;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 808; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKSLTKVNVKVPICGNNENEGSSRRNEEGSHPSNQSOQTAAQENKGEKSLTKSTPV 60  
Db 1 MFKSLTKVNVKVPICGNNENEGSSRRNEEGSHPSNQSOQTAAQENKGEKSLTKSTPV 60  
Qy 61 TSEEPHTNIQDKLSKNSGGDLTTPDPQNAAEPTGTVPQEKMDPGKEGSPNQKPPA 120  
Db 61 TSEEPHTNIQDKLSKNSGGDLTTPDPQNAAEPTGTVPQEKMDPGKEGSPNQKPPA 120  
Qy 121 APVINEYADAQLHNLVKRMQRORTALYKKKLVEGDLSSPEASPTAKTAVPPVKESDDKP 180  
Db 121 APVINEYADAQLHNLVKRMQRORTALYKKKLVEGDLSSPEASPTAKTAVPPVKESDDKP 180  
Qy 181 TEHYRLWLFVKVKMPLTEYLKRIKLPNSIDSYDRLYLMLLLVTLAYNWNCFIPLRL 240  
Db 181 TEHYRLWLFVKVKMPLTEYLKRIKLPNSIDSYDRLYLMLLLVTLAYNWNCFIPLRL 240  
Qy 241 VFPYQTADNIHYWLIADIICDIIYLYDMLFIQPLQFVRGGDIIVDSNELRKHRTSTKF 300



Db 541 KSVLYLPDGVCKGEGIKEMYYIKHGEVQVLGGPDGKVLVTLKAGSVFGEISLLAAGG 600  
Qy 601 GNRRTANVAVHGFANLLTLDKKTQLQELVHVPDSERILMKARVLLKQAKTAEATPPRK 660  
Db 601 GNRRTANVAVHGFANLLTLDKKTQLQELVHVPDSERILMKARVLLKQAKTAEATPPRK 660  
Qy 661 DLALLFPKPEETPKLFTKLLGGTGKASLARLLKLKREQAQKENSEGEGEKENEDKQ 720  
Db 661 DLALLFPKPEETPKLFTKLLGGTGKASLARLLKLKREQAQKENSEGEGEKENEDKQ 720  
Qy 721 KENEDKOKENEDKGENEDKKGREPEEKPLDRPECTASPIAVEEESHVVRTVLPRTGS 780  
Db 721 KENEDKOKENEDKGENEDKKGREPEEKPLDRPECTASPIAVEEESHVVRTVLPRTGS 780  
Qy 781 RQSLIISMAPSAEGGEEVLTIEVKEKAKQ 809  
Db 781 RQSLIISMAPSAEGGEEVLTIEVKEKAKQ 809

RESULT 5

AAE15986  
ID AAE15986 standard; protein; 809 AA.  
XX  
AC AAE15986;

XX  
DT 26-MAR-2002 (first entry)

XX  
DE Human CNG3B protein variant #4 (G682S).

XX  
KW Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;  
KW cyclic nucleotide-gated ion channel; contraceptive; vision disorder;  
KW male infertility; genetic defect; reporter-ligand interaction; CNG;  
KW viral infection; cancer; mutant; mutein; variant.

XX  
OS Homo sapiens.  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
FT Misc-difference 682  
FT /note= "Wild type Gly substituted with Ser"

XX  
PN WO200188090-A2.

XX  
PD 22-NOV-2001.

XX  
PF 15-MAY-2001; 2001WO-US015814.

XX  
PR 15-MAY-2000; 2000US-0204445P.

XX  
PR 14-MAY-2001; 2001US-0085582P.

XX  
PA (ICAG-) ICAGEN INC.

XX  
PI Creech CD, Jegla TJ;

XX  
DR WPI; 2002-089847/12.

XX  
PT New polypeptide, useful for screening for modulators of cyclic nucleotide  
PT -gated ion channels, comprises the isolated cyclic nucleotide-gated  
PT cation channel 3 beta subunit.

XX  
PS Disclosure; Page; 83pp; English.

XX  
CC The invention relates to human cyclic nucleotide-gated cation channel 3  
CC beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member  
CC of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms  
CC functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha  
CC subunits that are expressed in retina. CNG3B polypeptides are useful for  
CC screening modulators of CNGs which are useful as contraceptives and for  
CC treating various disorders involving cation channels, e.g. vision  
CC disorders and male infertility. Polynucleotides of the invention are  
CC useful for transfection of cells in vitro and in vivo, to correct  
CC acquired and inherited genetic defects, cancer and viral infections.

CC Sequences of the invention are useful as reporter molecules in assays and  
CC detection systems, to measure changes in cation concentration, membrane  
CC potential, current flow, ion flux, transcription, signal transduction,  
CC reporter-ligand interactions and second messenger concentrations, in  
CC vitro, in vivo and ex vivo. They are useful to construct models of CNGs  
CC in a computer system and for examining expression and regulation of  
CC cation channels. The present sequence is human CNG3B protein variant  
CC (G682S). Note: This sequence is not shown in the specification, but is  
CC derived from the human wild type CNG3B protein (SEQ ID NO:1) shown in Fig  
CC 4 of the specification (AAE15982)

XX  
SQ Sequence 809 AA;

Query Match 99.9%; Score 4228; DB 5; Length 809;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 808; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFKSLTKVNVKPIGNNENEQSSRRNEEGSHPNQSOQTAAQENKGEKSLTKSTPV 60  
Db 1 MFKSLTKVNVKPIGNNENEQSSRRNEEGSHPNQSOQTAAQENKGEKSLTKSTPV 60  
Qy 61 TSEEPHTNIQDKLSKNSSGDLTTNPDPPQNAAEPTGTVEOKEMDPGKGPNSPONKPPA 120  
Db 61 TSEEPHTNIQDKLSKNSSGDLTTNPDPPQNAAEPTGTVEOKEMDPGKGPNSPONKPPA 120  
Qy 121 APVINEYADAQLHNLVKRMQRQTALYKKLVGEGDLSSPEASPTAKPTAVPPVKESDDKP 180  
Db 121 APVINEYADAQLHNLVKRMQRQTALYKKLVGEGDLSSPEASPTAKPTAVPPVKESDDKP 180  
Qy 181 TEHYRLNFWKVKOMPLTEYLKRIKLPNSIDSYTDRLYLLMLLVTLAYNWCNFIPLRL 240  
Db 181 TEHYRLNFWKVKOMPLTEYLKRIKLPNSIDSYTDRLYLLMLLVTLAYNWCNFIPLRL 240  
Qy 241 VFYQTDADNTHYLIADIICDIIYLYDMLFQPLRQFVRGGDIIVDSNELRKHRTSTKF 300  
Db 241 VFYQTDADNTHYLIADIICDIIYLYDMLFQPLRQFVRGGDIIVDSNELRKHRTSTKF 300  
Qy 301 QLDVASIIPEDICYLFFGFNPMFRANRMLKYTSFFEFNHHLESIMDKAYIYRVIRTTGYL 360  
Db 301 QLDVASIIPEDICYLFFGFNPMFRANRMLKYTSFFEFNHHLESIMDKAYIYRVIRTTGYL 360  
Qy 361 LFIHINACVYVWASNYEGITTRWYVDGEGNEVLCYVWAVRTLIITIGGLPEQTLPFI 420  
Db 361 LFIHINACVYVWASNYEGITTRWYVDGEGNEVLCYVWAVRTLIITIGGLPEQTLPFI 420  
Qy 421 VFQLNFFSGVVFVSSLIQMRDVI GAATANQNTFRACMDDTIAYMNNYSIPKLQKRV 480  
Db 421 VFQLNFFSGVVFVSSLIQMRDVI GAATANQNTFRACMDDTIAYMNNYSIPKLQKRV 480  
Qy 481 TWYETWDSQRMDESLLKTLPTTVQLALADVNFISIISKVDLFKGCOTQMIYDMLLRL 540  
Db 481 TWYETWDSQRMDESLLKTLPTTVQLALADVNFISIISKVDLFKGCOTQMIYDMLLRL 540  
Qy 541 KSVLYLPDGVCKKGEGIKEMYYIKHGEVQVLGGPDGKVLVTLKAGSVFGEISLLAAGG 600  
Db 541 KSVLYLPDGVCKKGEGIKEMYYIKHGEVQVLGGPDGKVLVTLKAGSVFGEISLLAAGG 600  
Qy 601 GNRRTANVAVHGFANLLTLDKKTQLQELVHVPDSERILMKARVLLKQAKTAEATPPRK 660  
Db 601 GNRRTANVAVHGFANLLTLDKKTQLQELVHVPDSERILMKARVLLKQAKTAEATPPRK 660  
Qy 661 DLALLFPKPEETPKLFTKLLGGTGKASLARLLKLKREQAQKENSEGEGEKENEDKQ 720  
Db 661 DLALLFPKPEETPKLFTKLLGGTGKASLARLLKLKREQAQKENSEGEGEKENEDKQ 720  
Qy 721 KENEDKOKENEDKGENEDKKGREPEEKPLDRPECTASPIAVEEESHVVRTVLPRTGS 780  
Db 721 KENEDKOKENEDKGENEDKKGREPEEKPLDRPECTASPIAVEEESHVVRTVLPRTGS 780  
Qy 781 RQSLIISMAPSAEGGEEVLTIEVKEKAKQ 809  
Db 781 RQSLIISMAPSAEGGEEVLTIEVKEKAKQ 809







DE Novel human diagnostic protein #11960.  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
XX  
PR 23-AUG-2000; 2000US-00649167.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Dmanac RT, Liu C, Tang YT;  
XX  
XX WPI; 2001-639362/73.  
DR N-PSDB; AAS76156.  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
XX Claim 20; SEQ ID NO 42328; 103pp; English.  
XX  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (II) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have application in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: the sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 747 AA;  
XX  
Query Match 22.6%; Score 955; DB 4; Length 747;  
Best Local Similarity 32.8%; Pred. No. 5e-72;  
Matches 231; Conservative 17; Mismatches 34; Indels 422; Gaps 6;  
XX  
112 NSPQKPPAAVINEYADAQLHNLVKRMQROTALYKKKLVEGDLSSPEASPTAKTAVP 171  
DB 44 NSPQKPPAAVINEYADAQLHNLVKRMQROTALYKKKLVEGDLSSPEASPTAKTAVP 103  
XX  
172 PVKESDDKPTHEYRLWLFVKVKKMPLTEYLKRIKLPNSIDSYTORLYLLMLLVTLAYNW 231  
DB 104 PVKESDDKPTHEYRLWLFVKVKKMPLTEYLKRIKLPNSIDSYTORLYLLMLLVTLAYNW 163  
XX  
232 NCWFPIRLVPPYQTADNIHLYLADIICDIYLYDMLFIQPRIQFVRGGDI 284  
XX  
164 NCCFPIRLVPPYQTADNIHLYLADIICDIYLYDMLFIQPRIQFVRGGDIIRFQESYP 223  
XX  
285 -----VD-----SNELRKHYRTSTKQL----- 302  
XX  
224 SFSPIWFVDCDDPNLTSYLERPEDTENNYYLRQQLKCTWMPFEMLDQPLPMGQNGKIEVTS 283  
XX

QY 303 ----- 302  
DB 284 EEEEEEMAGDIKYLNHCKMKKEELISGKKLEDEGIEKENLATLEKIRKTQSGHLNVWVC 343  
QY 303 ----- 302  
DB 344 LSGGETTKPRNSGTGRRKESKQLKAGSQREWLVQVQIOTIGILMSEKAEMLTALYYTQHA 403  
QY 303 -----DVASIIIP----- 310  
DB 404 ARQFEGESKDLASCLQYSWRVQDNEGLSLNREQERLLELEQKAELEWEEVVEHROTLE 463  
QY 311 -----DICYLPFGFNPFRANRMLKYTSFFE----- 336  
DB 464 TMQNDLTTISHAVFQNGELKEQLAKLQTGFMKLANENMEITSTPQSEQHIKKPSEKLG 523  
QY 337 -----PNH 339  
DB 524 GLDSEEBALPLMPSIPEELESREAMVAFNLNSAVASABEEQAWPRGQLKEORGAMEKLQSH 583  
QY 340 HLESIMDKAYIR----- 352  
DB 584 FMELMQEKVDLKEOMEKLERRCIOLSGETDVIIHHTVPELEVSADVAPEGIHQPGGQ 643  
QY 353 ----- 352  
DB 644 GGDEGEAAGAAGAAGAGGIPPEGIVIIIGNDSSTHWPEDLPVGQDVDESDIDDP 703  
QY 353 ---VIRTTGYLLFILHINACVYVWASNYEGITGTRVWYDGE 393  
DB 704 DPVVIRTTGYLLFILHINACVYVWASNYEGITGTRVWYDGE 747

RESULT 11  
ABR39396  
ID ABR39396 standard; protein; 237 AA.  
XX  
AC ABR39396;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE Amino acid sequence of human betalb.  
XX  
KW OCN1; OCN2; betalb; CNG; human;  
KW olfactory cyclic nucleotide gated channel subunit.  
XX  
OS Homo sapiens.  
XX  
PN WO2003004611-A2.  
XX  
PD 16-JAN-2003.  
XX  
PF 08-JUL-2002; 2002WO-US021184.  
XX  
PR 06-JUL-2001; 2001US-0303140P.  
PR 10-DEC-2001; 2001US-0337154P.  
XX  
FA (SENO-) SENOMYX INC.  
XX  
PI Zoller MT, Xu H, Staszewski L, Moyer B, Pronin A, Adler JE;  
PI Servant G, Callamaras N;  
XX  
DR WPI; 2003-229406/22.  
DR N-PSDB; ABZ80565.  
XX  
PT Novel isolated nucleotide sequences encoding human OCN1, OCN2, beta 1b  
PT olfactory cyclic nucleotide gated (CNG) channel subunits, useful for  
PT identifying the CNG channel activators useful for enhancing smell.  
XX  
PS Disclosure; Page 86; 97pp; English.  
XX  
CC The present invention relates to a nucleotide sequences encoding human

CC OCN1, OCN2, or betalb olfactory cyclic nucleotide gated (CNG) channel  
 CC subunit, its action being an olfactory CNG channel activity modulator. A  
 CC host cell which expresses human OCN1, OCN2 and/or betalb is useful in a  
 CC mammalian cell-based assay for the profiling and screening of putative  
 CC modulators of a human olfactory cyclic nucleotide gated (CNG) channel.  
 CC The method is used to identify a compound as one which particularly  
 CC modulates CNG activity based on a detectable change in fluorescence. The  
 CC test cell expresses each of the human OCN1, human OCN2 and human betalb  
 CC subunits. A fluorescence plate reader or a voltage imaging plate are used  
 CC to monitor changes in fluorescence. The compounds that activate olfactory  
 CC CNG channel enhance smell and can be used to make foods more palatable  
 CC for individuals with attenuated olfactory function. The present sequence  
 CC represents the amino acid sequence of human betalb  
 XX  
 SQ Sequence 237 AA;

Query Match 21.4%; Score 906; DB 6; Length 237;  
 Best Local Similarity 72.8%; Pred. No. 1.4e-68;  
 Matches 171; Conservative 29; Mismatches 35; Indels 0; Gaps 0;  
 QY 417 LFEIVFOLLNFFSGVVFSSLIQMRDVIGATANQNYFRACMDDTIAYMNNYSIPKLVO 476  
 DB 1 LFEIVFOLLNFFSGVVFSSLIQMRDVIGATANQNYFRACMDDTIAYMNNYSIPKLVO 60  
 QY 477 KRVRTWYETWDSORMLDESLLKTLPTTVQLALADIVNFSIISKVDLFGCDTQMIYDM 536  
 DB 61 NRKVTWYETWDSORMLDESLLKTLPTTVQLALADIVNFSIISKVDLFGCDTQMIYDM 120  
 QY 537 LLRLKSVLYLPDGFVCKKGEIGKEMVYIKHGEVQVLGGPDGTVLTLKAGSVFGEISLL 596  
 DB 121 LKRLSVLYLPDGFVCKKGEIGKEMVYIKHGEVQVLGGPDGTVLTLKAGSVFGEISLL 180  
 QY 597 AAGGNNRTANVVAHGFANLLTDLKTLQELVHYPDSERILMKKARVLLKQKAK 651  
 DB 181 AVGGNNRTANVVAHGFANLLTDLKTLQELVHYPDSERILMKKARVLLKQKAK 235

## RESULT 12

ABP98584  
 ID ABP98584 standard; protein; 237 AA.

XX AC ABP98584;

DT 26-JUN-2003 (first entry)

XX Amino acid sequence of rat betalb.

DE OCN1, OCN2; betalb; CNG; rat;  
 KW olfactory cyclic nucleotide gated channel subunit.

XX Rattus sp.

XX WO2003004611-A2.

XX 16-JAN-2003.

XX 08-JUL-2002; 2002WO-US021184.

XX 06-JUL-2001; 2001US-0303140P.

XX 10-DEC-2001; 2001US-0337154P.

XX (SENO-) SENOMYX INC.

XX Zoller WT, Xu H, Staszewski L, Moyer B, Pronin A, Adler JE;

XX Servant G, Callamaras N;

XX WPI; 2003-229406/22.

XX Novel isolated nucleotide sequences encoding human OCN1, OCN2, beta 1b  
 PT olfactory cyclic nucleotide gated (CNG) channel subunits, useful for  
 XX identifying the CNG channel activators useful for enhancing smell.

XX Disclosure; Page 86; 97pp; English.

XX The present invention relates to a nucleotide sequences encoding human  
 CC OCN1, OCN2, or betalb olfactory cyclic nucleotide gated (CNG) channel  
 CC subunit, its action being an olfactory CNG channel activity modulator. A  
 CC host cell which expresses human OCN1, OCN2 and/or betalb is useful in a  
 CC mammalian cell-based assay for the profiling and screening of putative  
 CC modulators of a human olfactory cyclic nucleotide gated (CNG) channel.  
 CC The method is used to identify a compound as one which particularly  
 CC modulates CNG activity based on a detectable change in fluorescence. The  
 CC test cell expresses each of the human OCN1, human OCN2 and human betalb  
 CC subunits. A fluorescence plate reader or a voltage imaging plate are used  
 CC to monitor changes in fluorescence. The compounds that activate olfactory  
 CC CNG channel enhance smell and can be used to make foods more palatable  
 CC for individuals with attenuated olfactory function. The present sequence  
 CC represents the amino acid sequence of rat betalb  
 XX

SQ Sequence 237 AA;

Query Match 21.3%; Score 902; DB 6; Length 237;  
 Best Local Similarity 72.3%; Pred. No. 3e-68;

Matches 170; Conservative 30; Mismatches 35; Indels 0; Gaps 0;

QY 417 LFEIVFOLLNFFSGVVFSSLIQMRDVIGATANQNYFRACMDDTIAYMNNYSIPKLVO 476

DB 1 LFEIVFOLLNFFSGVVFSSLIQMRDVIGATANQNYFRACMDDTIAYMNNYSIPKLVO 60

QY 477 KRVRTWYETWDSORMLDESLLKTLPTTVQLALADIVNFSIISKVDLFGCDTQMIYDM 536

DB 61 NRKVTWYETWDSORMLDESLLKTLPTTVQLALADIVNFSIISKVDLFGCDTQMIYDM 120

QY 537 LLRLKSVLYLPDGFVCKKGEIGKEMVYIKHGEVQVLGGPDGTVLTLKAGSVFGEISLL 596

DB 121 LKRLSVLYLPDGFVCKKGEIGKEMVYIKHGEVQVLGGPDGTVLTLKAGSVFGEISLL 180

QY 597 AAGGNNRTANVVAHGFANLLTDLKTLQELVHYPDSERILMKKARVLLKQKAK 651

DB 181 AVGGNNRTANVVAHGFANLLTDLKTLQELVHYPDSERILMKKARVLLKQKAK 235

## RESULT 13

AAE15987  
 ID AAE15987 standard; protein; 694 AA.

XX AC AAE15987;

DT 26-MAR-2002 (first entry)

XX Human CNGA3 protein.

DE Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;  
 KW cyclic nucleotide-gated ion channel; contraceptive; vision disorder;  
 KW male infertility; genetic defect; reporter-ligand interaction; CNG;  
 KW viral infection; cancer; CNGA3 protein.

XX Homo sapiens.

XX WO200188090-A2.

XX 22-NOV-2001.

XX 15-MAY-2001; 2001WO-US015814.

XX 15-MAY-2000; 2000US-0204445P.

XX 14-MAY-2001; 2001US-00855828.

XX (ICAG-) ICAGEN INC.

XX Creech CD, Jegla TJ;

XX WPI; 2002-089847/12.

XX New polypeptide, useful for screening for modulators of cyclic nucleotide  
 PT -gated ion channels, comprises the isolated cyclic nucleotide-gated



PT cation channel 3 beta subunit.

XX Disclosure; Fig 1; 83pp; English.

XX The invention relates to human cyclic nucleotide-gated cation channel 3  
XX beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member  
XX of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms  
XX functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha  
XX subunits that are expressed in retina. CNG3B polypeptides are useful for  
XX screening modulators of CNGs which are useful as contraceptives and for  
XX treating various disorders involving cation channels, e.g. vision  
XX disorders and male infertility. Polynucleotides of the invention are  
XX useful for transfection of cells in vitro and in vivo, to correct  
XX acquired and inherited genetic defects, cancer and viral infections.  
XX Sequences of the invention are useful as reporter molecules in assays and  
XX detection systems, to measure changes in cation concentration, membrane  
XX potential, current flow, ion flux, transcription, signal transduction, in  
XX reporter-ligand interactions and second messenger concentrations, in  
XX vitro, in vivo and ex vivo. They are useful to construct models of CNGs  
XX in a computer system and for examining expression and regulation of  
XX cation channels. The present sequence is human CNGA3 protein

XX Sequence 694 AA;

Query Match 20.1%; Score 850; DB 5; Length 694;

Best Local Similarity 30.0%; Pred. No. 4.2e-63;

Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

QY	27	NEEGSHPSNQOQTAAQENKGEKSLKTPVTSEEPHTNIQDKLSKNSSGDLTNP	86
DB	5	NTQSHPS-----RTHLVK-----TSRDLNRAENGLSRAHSSSEETS--	43
QY	87	DPQAAEPTGTVEQKMDPGKEGNSPQNKPPAPVINEVADAOHLNLRMRORTALY	146
DB	44	---SVLPQ-GIATMRGLADSGQSFTGQ-----GIARLSRLIFLLRWAARH	87
QY	147	KKULVEGDLSP-----EASQTAKTAPVPVKESDDKPTHEYRLWFKVKMPL	197
DB	88	VHHDQGGPDSFPDRPRAELKEVSSQESNAQNVGSQEPADRG-----RSAP	136
QY	198	-----TEYLKRIKLPSNI-DSYDRLYLLWLLVTLAYNWNCFILRLVFPYQT	246
DB	137	AKCNTNTSNTTEEEKTKKDAIVDPSNSLYRRLTAIALPVFNWYLLICRACFDELQ	196
QY	247	ADNIHYMLIADIICDIYLYDMLFIQPLQFVRGDIIVDSNELRKHYRTSTKFDLDVAS	306
DB	197	SEYLMMLVLVDYSADVLVLVL-VRARTGLEQLMVSDTNRLWQHYKTTIQKLDVLS	255
QY	307	IIPFDICYLPFGFN-PMFRANRLKYTSFFPFNHHLESIMDKAVYRVIRTTGYLLFILH	365
DB	256	LVPTDLAYLVGTNTYPEVRNRLKFSRLFEFFDRTETRTNYPNNFRIGNLVLLIIHH	315
QY	366	INACVYVWASNYEGITRWYVDG-----EGNEYLCRYVAVRTLITIGGLPEPOTL	417
DB	316	WNACIYFAISKFIGFGDSWYPNISPEHGLRSKRYISLYWSTLTITIGETPPPVKD	375
QY	418	FEIVFQLNFFSGVVFSSLIQMRDVIQATANQVPRACDDTIAVMNYSIPKLKVK	477
DB	376	EYLFVVDVFLVGLVFIATIVGVNVSIMSNWNAEAEQAKIDSIKVMQFRKVKDLLET	435
QY	478	RVRTWEYTWDSQRLMDESLDKLTPTTVQALAIQDVNFSISKVDFLFGCDTQMIYDML	537
DB	436	RVIRWFYLMANKTVDKEVLSLDPDLKABIAINVHLDLTKKVRIFQDCEAGLLVELV	495
QY	538	LRLKSVLYLPDGFCKKGEIKEMVIKHGEVQVVGPDGKVLVTLKAGSVFGEISLLA	597
DB	496	LKLRPTVPSPGDYICKKGDIGKEMVIINEGLAVV-ADDGVTQFVVLSDGSYFGEISILN	554
QY	598	AGG---GNRRANTVVAHFANLLTLDKTLOEILVHVYDSEIRILMKAR-VLLKQK---A	650
DB	555	IKGSGNRRNTANRISIGYDLFCLSKDDLMLEALTEYPEAKKALEEKGROIKMDNLIDE	614
QY	651	KTAEATPPRKDALLFPFKETPKLFTLLGGTGKASLARLL-----KLKREQAQK	702

DB	615	EIARAGADPKDL-----EEKVEQLGSSL--DTLQTRFARLLAEYNATQMKORLSQLE	666
QY	703	KENSEGGE---EGKENEDKOKENEDKOK	728
DB	667	SQVKGKGRPLADGEVPGDATK-TEDKQ	694

RESULT 14

AAE38591

ID AAE38591 standard; protein; 694 AA.

AC AAE38591;

DT 04-DEC-2003 (first entry)

DE Human CNG channel alpha 3 potassium channel (KCQ2).

XX Human; urological disorder; urinary incontinence; gene therapy; cancer;  
KW kidney disorder; overactive; oversensitive bladder; dysfunction; bladder;  
KW urethra; overflow urinary incontinence; stress urinary incontinence;  
KW nervous system; prostatitis; benign prostatic hyperplasia; nephrotrophic;  
KW CNG channel alpha 3 potassium channel; KCQ2.

OS Homo sapiens.

PN WO2003061573-A2.

XX 31-JUL-2003.

PF 16-JAN-2003; 2003WO-US001450.

PR 18-JAN-2002; 2002US-0349511P.

PR 28-FEB-2002; 2002US-0360500P.

PR 15-MAR-2002; 2002US-0365041P.

PR 19-APR-2002; 2002US-0374063P.

PR 14-AUG-2002; 2002US-0403468P.

PR 27-SEP-2002; 2002US-0414262P.

PR 21-OCT-2002; 2002US-0419986P.

PR 05-NOV-2002; 2002US-0423809P.

PR 26-NOV-2002; 2002US-0429797P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Silos-Santiago I, Karicheti V;

XX WPI; 2003-598705/56.

XX N-PSDB; AAD58492.

XX Identifying a compound for treating urological disorders, for example  
XX urinary incontinence by assaying the ability of the compound to modulate  
XX the nucleic acid expression or polypeptide activity.

XX Disclosure; Page 159-160; Opp; English.

XX The present relates to a method for identifying a compound for treating  
XX urological disorders e.g., urinary incontinence including overactive/  
XX oversensitive bladder, overflow urinary incontinence, stress urinary  
XX incontinence caused by dysfunction of the bladder, urethra or central  
XX peripheral nervous system, prostatitis, benign prostatic hyperplasia,  
XX cancer of the prostate or kidney disorders. The method is also useful for  
XX modulating hyperplasia in a cell and treating a subject having a  
XX urological disorder. The invention is also used in gene therapy. The  
XX present sequence is human CNG channel alpha 3 potassium channel (KCQ2)

XX Sequence 694 AA;

Query Match

Best Local Similarity 20.1%; Score 850; DB 7; Length 694;

Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

QY	27	NEEGSHPSNQOQTAAQENKGEKSLKTPVTSEEPHTNIQDKLSKNSSGDLTNP	86
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 27, 2005, 20:58:17 ; Search time 1171 Seconds  
(without alignments)  
228.745 Million cell updates/sec

Title: US-09-855-828-1  
Perfect score: 4234  
Sequence: 1 MFKSLTKVKNVKPIGENNEN.....PSABGGSEVLTVIEVKEKAKQ 809

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
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- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
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- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4234	100.0	809	11	US-09-855-828-1
2	4228	99.9	809	11	US-09-855-828-1
3	906	21.4	237	15	US-10-189-507-11
4	902	21.3	237	15	US-10-189-507-7
5	850	20.1	694	10	US-09-842-758-75
6	850	20.1	694	11	US-09-855-828-14
7	850	20.1	694	14	US-10-345-680-26
8	850	20.1	694	15	US-10-174-333-75
9	829	19.6	663	14	US-10-029-677-16
10	825.5	19.5	664	14	US-10-029-677-24
11	820.5	19.4	664	14	US-10-029-677-2
12	820	19.4	732	10	US-09-842-758-73
13	820	19.4	732	14	US-10-029-677-15

14	820	19.4	732	15	US-10-174-333-73	Sequence 73, Appl
15	819.5	19.4	664	9	US-09-735-927-2	Sequence 2, Appl
16	819.5	19.4	664	13	US-10-034-843-2	Sequence 2, Appl
17	819.5	19.4	664	14	US-10-168-651-7	Sequence 7, Appl
18	819.5	19.4	664	14	US-10-114-153-18	Sequence 18, Appl
19	818.5	19.3	664	9	US-09-735-927-4	Sequence 4, Appl
20	817	19.3	690	11	US-09-855-828-15	Sequence 15, Appl
21	804	19.0	664	14	US-10-029-677-18	Sequence 18, Appl
22	804	19.0	664	14	US-10-087-217-2	Sequence 2, Appl
23	804	19.0	664	14	US-10-295-573-8	Sequence 8, Appl
24	802	18.9	664	14	US-10-295-573-5	Sequence 5, Appl
25	795	18.8	664	14	US-10-087-217-4	Sequence 4, Appl
26	791	18.7	664	14	US-10-087-217-6	Sequence 6, Appl
27	791	18.7	664	14	US-10-295-573-6	Sequence 6, Appl
28	782	18.5	664	14	US-10-087-217-8	Sequence 8, Appl
29	777.5	18.4	664	14	US-10-029-677-17	Sequence 17, Appl
30	773	18.3	634	14	US-10-295-573-7	Sequence 7, Appl
31	656	15.5	578	10	US-09-842-758-28	Sequence 28, Appl
32	656	15.5	578	15	US-10-174-333-28	Sequence 28, Appl
33	655	15.5	575	9	US-09-735-932-2	Sequence 2, Appl
34	655	15.5	575	9	US-09-927-267-1	Sequence 1, Appl
35	655	15.5	575	10	US-09-842-758-30	Sequence 30, Appl
36	655	15.5	575	14	US-10-207-951-2	Sequence 2, Appl
37	655	15.5	575	15	US-10-174-333-30	Sequence 30, Appl
38	653	15.4	575	16	US-10-311-624-1	Sequence 1, Appl
39	640	15.1	575	9	US-09-735-932-4	Sequence 16, Appl
40	640	15.1	575	9	US-09-927-267-16	Sequence 74, Appl
41	640	15.1	575	10	US-09-842-758-74	Sequence 74, Appl
42	640	15.1	575	15	US-10-174-333-74	Sequence 5, Appl
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45	437	10.3	239	15	US-10-189-507-12	

ALIGNMENTS

RESULT 1

US-09-855-828-1  
; Sequence 1, Application US/09855828  
; Publication No. US20040137433A1  
; GENERAL INFORMATION:  
; APPLICANT: Cretech, Christopher D.  
; APPLICANT: Jegla, Timothy J.  
; APPLICANT: ICAGEN, Inc.  
; TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel  
; FILE REFERENCE: 018512-006010US  
; CURRENT APPLICATION NUMBER: US/09/855,828  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: US 60/204,445  
; PRIOR FILING DATE: 2000-05-15  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 809  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human cyclic nucleotide-gated cation channel (CNG)  
; OTHER INFORMATION: 3B (CNG3B)  
; US-09-855-828-1

Query Match	100.0%	Score 4234;	DB 11;	Length 809;
Best Local Similarity	100.0%	Pred. No. 3.8e-301;		
Matches 809;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	
Qy	1	MFKSLTKVKNVKPIGENNENEQSSRRNEGSHPSNQSQTTAQEENKGEKSLTKSTPV	60	
Db	1	MFKSLTKVKNVKPIGENNENEQSSRRNEGSHPSNQSQTTAQEENKGEKSLTKSTPV	60	
Qy	61	TSEEPHTNIQDKLSKKNSGDLTTNPDQNAAEPTGTVPEQKMDPKGEGNSQNKPPA	120	
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QY 181 TEHYRLLLWFKVKOMPLTEYLKRIKLPNSIDSYTDRLYLLWLLVTLAYNNWCWFIPLRL 240  
DB 181 TEHYRLLLWFKVKOMPLTEYLKRIKLPNSIDSYTDRLYLLWLLVTLAYNNWCWFIPLRL 240  
QY 241 VFPYQTADNIHYWLIADIIICDIIYLYDMLFIQPLQFVRGGDIIIVDSNELRKHRTSTKF 300  
DB 241 VFPYQTADNIHYWLIADIIICDIIYLYDMLFIQPLQFVRGGDIIIVDSNELRKHRTSTKF 300  
QY 301 QLDVASIIPFDICYLFFGFNPMFRANRMLKYTSFFEFNHLESIMDKAYIYRVIRTTGYL 360  
DB 301 QLDVASIIPFDICYLFFGFNPMFRANRMLKYTSFFEFNHLESIMDKAYIYRVIRTTGYL 360  
QY 361 LFIHINACVYVWASNYEGIGTTRWYDGEVQLGPGDGTGKVLVTLKAGSVFGEISLLAAGG 420  
DB 361 LFIHINACVYVWASNYEGIGTTRWYDGEVQLGPGDGTGKVLVTLKAGSVFGEISLLAAGG 420  
QY 421 VFQLLNFFSGVVFSSLIQOMRDVIGAATANONYFRACMDDTIAYMNNYSIPKLVKQKVR 480  
DB 421 VFQLLNFFSGVVFSSLIQOMRDVIGAATANONYFRACMDDTIAYMNNYSIPKLVKQKVR 480  
QY 481 TWYEYTWDSQRMLESDDLKTLPTTVQLALAIQVNFSSIIISKVDLFKGCDDTQMIYDMLLRL 540  
DB 481 TWYEYTWDSQRMLESDDLKTLPTTVQLALAIQVNFSSIIISKVDLFKGCDDTQMIYDMLLRL 540  
QY 541 KSVLYLPGDFVCKGKEIGKEMYIIKHGEVQVLGPGDGTGKVLVTLKAGSVFGEISLLAAGG 600  
DB 541 KSVLYLPGDFVCKGKEIGKEMYIIKHGEVQVLGPGDGTGKVLVTLKAGSVFGEISLLAAGG 600  
QY 601 GNRRTANVAHGFANLLTLDKKTLQELVHYPDSEIRILMKKARVLLKOKAKTAEATPPRK 660  
DB 601 GNRRTANVAHGFANLLTLDKKTLQELVHYPDSEIRILMKKARVLLKOKAKTAEATPPRK 660  
QY 661 DLALLFPKKEETPKLFKTLGGTGKASLARLLKLKREQAQKENSEGEGEENEDKQ 720  
DB 661 DLALLFPKKEETPKLFKTLGGTGKASLARLLKLKREQAQKENSEGEGEENEDKQ 720  
QY 721 KENEDKQKENEKDKGKEPEEKPLDRPECTASPIAVEEPHSHVRRVTLPRGTS 780  
DB 721 KENEDKQKENEKDKGKEPEEKPLDRPECTASPIAVEEPHSHVRRVTLPRGTS 780  
QY 781 QSLIISMAPSABGGEVLTIEVKEKAKQ 809  
DB 781 QSLIISMAPSABGGEVLTIEVKEKAKQ 809

## RESULT 2

US-09-855-828-13  
; Sequence 13, Application US/09855828  
; Publication No. US20040137433A1  
; GENERAL INFORMATION:  
; APPLICANT: Creech, Christopher D.  
; APPLICANT: Jegla, Timothy J.  
; APPLICANT: ICAGEN, Inc.  
; TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel  
; FILE REFERENCE: 018512-006010US  
; CURRENT APPLICATION NUMBER: US/09/855, 828  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: US 60/204,445  
; PRIOR FILING DATE: 2000-05-15  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 809  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: CNG3B  
US-09-855-828-13

Query Match 99.9%; Score 4228; DB 11; Length 809;  
Best Local Similarity 99.9%; Pred. No. 1.1e-300;  
Matches 808; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MPKSLTKVNVKXPIGENNENEQSSRRNERGSHPSNOSQOQTAAEENKGBEKSILKTSTPV 60  
DB 1 MPKSLTKVNVKXPIGENNENEQSSRRNERGSHPSNOSQOQTAAEENKGBEKSILKTSTPV 60  
QY 61 TSEEPHTNIQDKLSKNSSGDLTTNPDPQNAAEPTGTVPQEKEMDPGKGGPNSPQNKPAA 120  
DB 61 TSEEPHTNIQDKLSKNSSGDLTTNPDPQNAAEPTGTVPQEKEMDPGKGGPNSPQNKPAA 120  
QY 121 APVINEYADAQLHNLVKRMQRORTALYKKKLVEGDLSSPEASPTAKPTAVPPVKESDDKP 180  
DB 121 APVINEYADAQLHNLVKRMQRORTALYKKKLVEGDLSSPEASPTAKPTAVPPVKESDDKP 180  
QY 181 TEHYRLLLWFKVKOMPLTEYLKRIKLPNSIDSYTDRLYLLWLLVTLAYNNWCWFIPLRL 240  
DB 181 TEHYRLLLWFKVKOMPLTEYLKRIKLPNSIDSYTDRLYLLWLLVTLAYNNWCWFIPLRL 240  
QY 241 VFPYQTADNIHYWLIADIIICDIIYLYDMLFIQPLQFVRGGDIIIVDSNELRKHRTSTKF 300  
DB 241 VFPYQTADNIHYWLIADIIICDIIYLYDMLFIQPLQFVRGGDIIIVDSNELRKHRTSTKF 300  
QY 301 QLDVASIIPFDICYLFFGFNPMFRANRMLKYTSFFEFNHLESIMDKAYIYRVIRTTGYL 360  
DB 301 QLDVASIIPFDICYLFFGFNPMFRANRMLKYTSFFEFNHLESIMDKAYIYRVIRTTGYL 360  
QY 361 LFIHINACVYVWASNYEGIGTTRWYDGEVQLGPGDGTGKVLVTLKAGSVFGEISLLAAGG 420  
DB 361 LFIHINACVYVWASNYEGIGTTRWYDGEVQLGPGDGTGKVLVTLKAGSVFGEISLLAAGG 420  
QY 421 VFQLLNFFSGVVFSSLIQOMRDVIGAATANONYFRACMDDTIAYMNNYSIPKLVKQKVR 480  
DB 421 VFQLLNFFSGVVFSSLIQOMRDVIGAATANONYFRACMDDTIAYMNNYSIPKLVKQKVR 480  
QY 481 TWYEYTWDSQRMLESDDLKTLPTTVQLALAIQVNFSSIIISKVDLFKGCDDTQMIYDMLLRL 540  
DB 481 TWYEYTWDSQRMLESDDLKTLPTTVQLALAIQVNFSSIIISKVDLFKGCDDTQMIYDMLLRL 540  
QY 541 KSVLYLPGDFVCKGKEIGKEMYIIKHGEVQVLGPGDGTGKVLVTLKAGSVFGEISLLAAGG 600  
DB 541 KSVLYLPGDFVCKGKEIGKEMYIIKHGEVQVLGPGDGTGKVLVTLKAGSVFGEISLLAAGG 600  
QY 601 GNRRTANVAHGFANLLTLDKKTLQELVHYPDSEIRILMKKARVLLKOKAKTAEATPPRK 660  
DB 601 GNRRTANVAHGFANLLTLDKKTLQELVHYPDSEIRILMKKARVLLKOKAKTAEATPPRK 660  
QY 661 DLALLFPKKEETPKLFKTLGGTGKASLARLLKLKREQAQKENSEGEGEENEDKQ 720  
DB 661 DLALLFPKKEETPKLFKTLGGTGKASLARLLKLKREQAQKENSEGEGEENEDKQ 720  
QY 721 KENEDKQKENEKDKGKEPEEKPLDRPECTASPIAVEEPHSHVRRVTLPRGTS 780  
DB 721 KENEDKQKENEKDKGKEPEEKPLDRPECTASPIAVEEPHSHVRRVTLPRGTS 780  
QY 781 QSLIISMAPSABGGEVLTIEVKEKAKQ 809  
DB 781 QSLIISMAPSABGGEVLTIEVKEKAKQ 809

## RESULT 3

US-10-189-507-11  
; Sequence 11, Application US/10189507  
; Publication No. US20030228633A1  
; GENERAL INFORMATION:  
; APPLICANT: ZOLLER, MARK  
; APPLICANT: XU, HONG  
; APPLICANT: STASZEWSKI, IENA  
; APPLICANT: MOYER, BRYAN  
; APPLICANT: PRONIN, ALEXY  
; APPLICANT: ADLER, JON ELLIOT

APPLICANT: SERVANT, GUY  
APPLICANT: CALLAMARAS, NICHOLAS  
TITLE OF INVENTION: EXPRESSION OF FUNCTIONAL HUMAN OLFACTORY CYCLIC  
TITLE OF INVENTION: NUCLEOTIDE GATED (CNG) CHANNEL IN RECOMBINANT HOST  
TITLE OF INVENTION: CELLS AND USE THEREOF IN CELL BASED ASSAYS TO IDENTIFY  
TITLE OF INVENTION: SMELL MODULATORS  
FILE REFERENCE: 078003-0291567  
CURRENT APPLICATION NUMBER: US/10/189,507  
CURRENT FILING DATE: 2003-02-12  
PRIOR APPLICATION NUMBER: 60/303,140  
PRIOR FILING DATE: 2001-07-06  
PRIOR APPLICATION NUMBER: 60/337,154  
PRIOR FILING DATE: 2001-12-10  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 237  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-189-507-11

Query Match 21.4%; Score 906; DB 15; Length 237;  
Best Local Similarity 72.8%; Pred. No. 3.9e-58;  
Matches 171; Conservative 29; Mismatches 35; Indels 0; Gaps 0;  
Qy 417 LFEIVFOLLNPFSGVVFSSLIQMRDVGIGATANQNYFRACMDDTIAYMNNYSIPKLQV 476  
Db 1 LFEIVFOLLNFTGTGFAFVSMIGMRDVVGAATAGQTYRSCMDSTVKYMFYKIPKSVQ 60  
Qy 477 KRVTWYETWDSQRMDESLTKLPTTVQALAIADVNFSIIISKVDLFGKCDTQMIYDM 536  
Db 61 NRVTWYETWHSQGMDESELMVQLDPKMRDLDAIDVNNIVSKVALFQCDRQMIYDM 120  
Qy 537 LLRLKSVLYLPDGFVCKKGEGIKEMYIIKHGEVQVLGPGDGTKVLTAKGSVFGEISLL 596  
Db 121 LKRLRSVYLPNDVYCKKGEGIKEMYIIQAGQVQVLGPGDGKSVLTLKAGSVFGEISLL 180  
Qy 597 AAGGNRRRTANVAHGFANLLTLDKKTLQELVHYPDSERILMKARVLLKQKAK 651  
Db 181 AVGGNRRRTANVAHGFNTLFDLKKDLNEILVHYPESQKLLRKKARRMLRNNK 235

RESULT 4  
US-10-189-507-7  
Sequence 7, Application US/10189507  
Publication No. US20030228633A1  
GENERAL INFORMATION:  
APPLICANT: ZOLLER, MARK  
APPLICANT: XU, HONG  
APPLICANT: STASZEWSKI, LENA  
APPLICANT: MOYER, BRYAN  
APPLICANT: PRONIN, ALEX  
APPLICANT: ADLER, JON ELLIOT  
APPLICANT: SERVANT, GUY  
APPLICANT: CALLAMARAS, NICHOLAS  
TITLE OF INVENTION: EXPRESSION OF FUNCTIONAL HUMAN OLFACTORY CYCLIC  
TITLE OF INVENTION: NUCLEOTIDE GATED (CNG) CHANNEL IN RECOMBINANT HOST  
TITLE OF INVENTION: CELLS AND USE THEREOF IN CELL BASED ASSAYS TO IDENTIFY  
TITLE OF INVENTION: SMELL MODULATORS  
FILE REFERENCE: 078003-0291567  
CURRENT APPLICATION NUMBER: US/10/189,507  
CURRENT FILING DATE: 2003-02-12  
PRIOR APPLICATION NUMBER: 60/303,140  
PRIOR FILING DATE: 2001-07-06  
PRIOR APPLICATION NUMBER: 60/337,154  
PRIOR FILING DATE: 2001-12-10  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 237  
TYPE: PRT  
ORGANISM: Rattus sp.  
US-10-189-507-7

Query Match 21.3%; Score 902; DB 15; Length 237;  
Best Local Similarity 72.3%; Pred. No. 7.7e-58;  
Matches 170; Conservative 30; Mismatches 35; Indels 0; Gaps 0;  
Qy 417 LFEIVFOLLNPFSGVVFSSLIQMRDVGIGATANQNYFRACMDDTIAYMNNYSIPKLQV 476  
Db 1 LFEIVFOLLNFTGTGFAFVSMIGMRDVVGAATAGQTYRSCMDSTVKYMFYKIPKSVQ 60  
Qy 477 KRVTWYETWDSQRMDESLTKLPTTVQALAIADVNFSIIISKVDLFGKCDTQMIYDM 536  
Db 61 NRVTWYETWHSQGMDESELMVQLDPKMRDLDAIDVNNIVSKVALFQCDRQMIYDM 120  
Qy 537 LLRLKSVLYLPDGFVCKKGEGIKEMYIIKHGEVQVLGPGDGTKVLTAKGSVFGEISLL 596  
Db 121 LKRLRSVYLPNDVYCKKGEGIKEMYIIQAGQVQVLGPGDGKSVLTLKAGSVFGEISLL 180  
Qy 597 AAGGNRRRTANVAHGFANLLTLDKKTLQELVHYPDSERILMKARVLLKQKAK 651  
Db 181 AVGGNRRRTANVAHGFNTLFDLKKDLNEILVHYPESQKLLRKKARRMLRNNK 235

RESULT 5  
US-09-842-758-75  
Sequence 75, Application US/09842758  
Publication No. US20030083244A1  
GENERAL INFORMATION:  
APPLICANT: Vernet, Corine A. M.  
APPLICANT: Fernandes, Elma R.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Shimkets, Richard A  
APPLICANT: Malyankar, Uriel M  
APPLICANT: Boldog, Ferenc L  
APPLICANT: Zerhusen, Bryan D  
APPLICANT: Spytek, Kimberly A  
APPLICANT: Majumder, Kumud  
APPLICANT: Tchernev, Velizar T  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Patturajan, Meera  
APPLICANT: Burgess, Catherine E  
APPLICANT: Gangolli, Esha A  
APPLICANT: Smithson, Glennda  
APPLICANT: MacDougall, John R  
APPLICANT: Taupier, Raymond J  
APPLICANT: Grosse, William M  
APPLICANT: Edward, Szekeres S  
APPLICANT: Alsobrook II, John P  
TITLE OF INVENTION: No. US20030083244A1el Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 15966-783  
CURRENT APPLICATION NUMBER: US/09/842,758  
CURRENT FILING DATE: 2001-04-25  
PRIOR APPLICATION NUMBER: 60/200,158  
PRIOR FILING DATE: 2000-04-26  
PRIOR APPLICATION NUMBER: 60/200,613  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 60/200,780  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 60/201,006  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/201,007  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/201,236  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/201,238  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/201,186  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 60/201,474  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: 60/201,508  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: 60/220,591

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; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/232,678
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/263,217
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/265,160
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-842-758-75

Query Match      20.1%; Score 850; DB 10; Length 694;
Best Local Similarity 30.0%; Pred. No. 2.3e-53;
Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

Qy 27 NEEGSHPSNQSQOQTAAQENKGEESLKTKSTPVTSEEPHTNIQDKLSKNSSGDLTTNP 86
Db 5 NTQYSHPS-----RTHLKVK-----TSDRLNRAENGLSRAHSSEETS-- 43

Qy 87 DPQNAEPTGTVPROKEMDPKGEPNSPQNKPPAAPVINEYADAOQLHNLVKRMORTALY 146
Db 44 ---SVLQP-GIAMETRGADSGQSFTGQ-----GIARLSRLIFLLRWAARH 87

Qy 147 KKKLVEGDLSP-----EASPTAKPTAVPPVKESDDKPTHEYHYRLWLFVKVMPL 197
Db 88 VHQDQGPDPDFPRGAELEKVSQESNAQANVGSEPADRG-----RSAW-----PL 136

Qy 198 -----TEYLKRIKLPSNI-DSYTDRLYLLMLLVLTAYNNWCWFIPRLVPPYQT 246
Db 137 AKCNTNTSNTTEBEKTKKDAIVDPSSNLYRWLTAIALPVFNWYLLICRACFDELQ 196

Qy 247 ADNIHYLIADIICDIYLYDMLFIQPRLOFVRGGDIIVDSNELRKHRTSTFKQDVLAS 306
Db 197 SEYLMWLVLVDSADVLVYLDVL-VRARTGFLEQGLMVSQDNLRLQWYKTTTQFKLDVLS 255

Qy 307 IIPFDICYLFPGFN-PMFRANRMLKYTSFFEPFNHLESIMDKAVIYRVIRTTGYLLFILH 365
Db 256 LVPTDLAYLKVGTYNPEVRFNRLKFSRLFEFDRTETRTNPNNFRIGNLVLYLIIH 315

Qy 366 INACVYVWASNYEGIGTRWVYDG-----EGNEYLRCYVWAVRVLITIGGLPEPQTL 417
Db 316 WNACIYFAISKFIGTDSWVYFNISIPHEGRLSRKYIYSLYWSLTLTITIGETPPVKD 375

Qy 418 FEIVFQLNFFSGVVFESSLIGQMRDVIGATANQNYFRACMDDTIAYMNNYSIPKLVQK 477
Db 376 EYLFVVDVFLVGLVIFATIVGNVGMISNMNASRAEFQAKIDSIKQYQWFRKVTKDLET 435

Qy 478 RVRTWYETWDSQRMDESLLKTLPTTVQALALADVNFSSIISKVDLFKGCQDTQMIYDML 537
Db 436 RVIRWFDYLVANKTVDEKEVLSKLPDLKAEIAINVHLDTLKKVIRIQQCEAGLIVELV 495

Qy 538 LRLKSVLYLPGDFVCKKGEIGKEMYIIKHGEVOVLGGPDGTVKLVLTAKAGSVFGEISLAA 597
Db 496 LKLRPTVFSQDYGICCKGDIKEMYIINEGLAVV-ADGVTQFVVLSDGVSFGEISILN 554

Qy 598 AGG---GNRRTANVVAHGAFANLLTKKTLOEILVHYPPDSERILMKKAR-VLLKQK---A 650
Db 555 IKGSGKGNRRNTANIRSIGYSDFLSKDLDLMEALTEYPEAKKALEEKGRIQILMKDNLIDE 614

Qy 651 KTAEATPPRKDALLFPPEKETPKLFTLLGGTGKASLARLL-----KLKREOAQK 702
Db 615 ELARAGADPKDL-----BEKVQLGSSL--DTLQTFPALLAEYNAQWKKQRLSLE 666

Qy 703 KENSEGEE---EGKNEDEKQKNEDEKQK 728
Db 667 SOVKGGGDKPLADGEVFGATK-TEDKQK 694

RESULT 6
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```
US-09-855-828-14
; Sequence 14, Application US/09855828
; Publication No. US20040137433A1
; GENERAL INFORMATION:
; APPLICANT: Creech, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: ICAGEN, INC.
; TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel
; FILE REFERENCE: 018512-006010US
; CURRENT APPLICATION NUMBER: US/09/855,828
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/204,445
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CNGA1
US-09-855-828-14

Query Match      20.1%; Score 850; DB 11; Length 694;
Best Local Similarity 30.0%; Pred. No. 2.3e-53;
Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

Qy 27 NEEGSHPSNQSQOQTAAQENKGEESLKTKSTPVTSEEPHTNIQDKLSKNSSGDLTTNP 86
Db 5 NTQYSHPS-----RTHLKVK-----TSDRLNRAENGLSRAHSSEETS-- 43

Qy 87 DPQNAEPTGTVPEQKEMDPKGEPNSPQNKPPAAPVINEYADAOQLHNLVKRMORTALY 146
Db 44 ---SVLQP-GIAMETRGADSGQSFTGQ-----GIARLSRLIFLLRWAARH 87

Qy 147 KKKLVEGDLSP-----EASPTAKPTAVPPVKESDDKPTHEYHYRLWLFVKVMPL 197
Db 88 VHQDQGPDPDFPRGAELEKVSQESNAQANVGSEPADRG-----RSAW-----PL 136

Qy 198 -----TEYLKRIKLPSNI-DSYTDRLYLLMLLVLTAYNNWCWFIPRLVPPYQT 246
Db 137 AKCNTNTSNTTEBEKTKKDAIVDPSSNLYRWLTAIALPVFNWYLLICRACFDELQ 196

Qy 247 ADNIHYLIADIICDIYLYDMLFIQPRLOFVRGGDIIVDSNELRKHRTSTFKQDVLAS 306
Db 197 SEYLMWLVLVDSADVLVYLDVL-VRARTGFLEQGLMVSQDNLRLQWYKTTTQFKLDVLS 255

Qy 307 IIPFDICYLFPGFN-PMFRANRMLKYTSFFEPFNHLESIMDKAVIYRVIRTTGYLLFILH 365
Db 256 LVPTDLAYLKVGTYNPEVRFNRLKFSRLFEFDRTETRTNPNNFRIGNLVLYLIIH 315

Qy 366 INACVYVWASNYEGIGTRWVYDG-----EGNEYLRCYVWAVRVLITIGGLPEPQTL 417
Db 316 WNACIYFAISKFIGTDSWVYFNISIPHEGRLSRKYIYSLYWSLTLTITIGETPPVKD 375

Qy 418 FEIVFQLNFFSGVVFESSLIGQMRDVIGATANQNYFRACMDDTIAYMNNYSIPKLVQK 477
Db 376 EYLFVVDVFLVGLVIFATIVGNVGMISNMNASRAEFQAKIDSIKQYQWFRKVTKDLET 435

Qy 478 RVRTWYETWDSQRMDESLLKTLPTTVQALALADVNFSSIISKVDLFKGCQDTQMIYDML 537
Db 436 RVIRWFDYLVANKTVDEKEVLSKLPDLKAEIAINVHLDTLKKVIRIQQCEAGLIVELV 495

Qy 538 LRLKSVLYLPGDFVCKKGEIGKEMYIIKHGEVOVLGGPDGTVKLVLTAKAGSVFGEISLAA 597
Db 496 LKLRPTVFSQDYGICCKGDIKEMYIINEGLAVV-ADGVTQFVVLSDGVSFGEISILN 554

Qy 598 AGG---GNRRTANVVAHGAFANLLTKKTLOEILVHYPPDSERILMKKAR-VLLKQK---A 650
Db 555 IKGSGKGNRRNTANIRSIGYSDFLSKDLDLMEALTEYPEAKKALEEKGRIQILMKDNLIDE 614

Qy 651 KTAEATPPRKDALLFPPEKETPKLFTLLGGTGKASLARLL-----KLKREOAQK 702
Db 615 ELARAGADPKDL-----BEKVQLGSSL--DTLQTFPALLAEYNAQWKKQRLSLE 666

Qy 703 KENSEGEE---EGKNEDEKQKNEDEKQK 728
Db 667 SOVKGGGDKPLADGEVFGATK-TEDKQK 694

RESULT 6
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Db 615 ELARAGADPKDL-----EKEVEQLGSSL--DTLQTRFARLLAEYNATQMKMKQRLSQLE 666
Qy 703 KENSEGEE---EGKENEDKOKENEDKQK 728
Db 667 SQVKGKGDPLADGEVPGDATK-TEDKQK 694

RESULT 7
US-10-345-680-26
; Sequence 26, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Siles-Santiago, Inmaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012PIRNM, ONNI
; CURRENT APPLICATION NUMBER: US/10/345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-345-680-26

Query Match 20.1%; Score 850; DB 14; Length 694;
Best Local Similarity 30.0%; Pred. No. 2.3e-53;
Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

Qy 27 NEEGSHPSNCSQQTAAQENKGEKSLKTKSTPTVSTSEPHNTIQDKLSKKNSSGDLTNP 86
Db 5 NTQVSHPS-----RTHLKVK-----TSRDRLNRAENGLSRAHSSSEETS-- 43
Qy 87 DPQNAASPFTGTVPRKEMDPKGPSPQNPKPAPVINEVADALHNLVKRMQRTALY 146
Db 44 ---SVLOP-GIAMETRGLADSGQSFTGQ-----GIARLSRLIFLLRWARH 87
Qy 147 KKKLVEGDLSP-----EASPTAKPTAVPPVKESDDKPTHEYRLWFKVKMPL 197
Db 88 VHQDQGPDPDFRFRGAELKEVSSQESNAQNVGSQEPADRG-----RSAAW-----PL 136
Qy 198 -----TEYLRKRLKPNIS--DSYTDRLYLWLLVLTAYNWCWFPLRLVFPYQT 246
Db 137 AKCNTNTSNTEEEKTKKKDAIVVDFSSNLYRWLTAIALPVPYNNYLLICRACFDELQ 196
Qy 247 ADNIHWLIADICDIIVLYDMLFIQPLQFVRGDIIVDSNELRKHVRTSTKEFQDVAS 306
Db 197 SEYLMMLVLDYSADVLVLDVL--VRARTGLEQMLVSDTNRLWQHVKITTKQKLDVLS 255
Qy 307 IIPEDICYLPFGFN-PMFRANRMLKYTSFFEFNHLESIMDKAYIYRVRTTGYLLFILH 365
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Db 256 LVPTDLAYLKGVTNYPEVRFNRLKFSRLFFDFDTETRTNYPNNFRIGNLVLYLIIH 315
Qy 366 INACVYVWASNYEGIGTTRWVYDG-----EGNEYLRCYVWAVRTLITIGLPEPQTL 417
Db 316 WNACIYFAISKFIQFGTDSWYFNISPEHGRLSRKYIYSYLWSTLTTLTIGETPPVKD 375
Qy 418 FEIVFQLNFFSGVVFSSLIQMRDVIQAATANQNYFRACMDDTIAYMNNYSIPKLQK 477
Db 376 EBYLFVVVDVLVGLVIFATIVGVNVMISNNWASRAEFQAKIDSIKQYMQPRKVKTDLET 435
Qy 478 RVRTWYETWDSORMLDESLLKTLPTTVQALALDVNFSIISKVDLFGCDTQMIYML 537
Db 436 RVIRMFYLMANKKTVDKEVLSPLDKLKAIAINVHLDLTKKVRIFQDCEAGLVEIV 495
Qy 538 LRLKSLVLPDGFVCKKGEIGKEMVIIKHGVQVVLGGDGTGKVLVTLKAGSVFGSISLLA 597
Db 496 LKLRPTVSPGDIYCKKGDIGKEMVIINEGKLVV-ADGVTQFVVLSDGSVFGSISLN 554
Qy 598 AGG---GNRRTANVAVHGFANLLTLDKKTQLQEIIVHVPDSERILMKKAR-VLLKQK---A 650
Db 555 IKGSKSGNRRTANIRSIGYSLFCLSKDDLMEALTEYPEAKKALEEKGRQILMKDNLIDE 614
Qy 651 KTAETATPRKDLALLFPKBPETPKLFKTLGGTGKASLARLL-----KUKREQAQK 702
Db 615 ELARAGADPKDL-----EKEVEQLGSSL--DTLQTRFARLLAEYNATQMKMKQRLSQLE 666
Qy 703 KENSEGEE---EGKENEDKOKENEDKQK 728
Db 667 SQVKGKGDPLADGEVPGDATK-TEDKQK 694
```

```
RESULT 8
US-10-174-333-75
; Sequence 75, Application US/10174333
; Publication No. US20040029220A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Geryach, Valerie
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Raetelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Grosse, William M.
; APPLICANT: Szekeres, Edward S.
; APPLICANT: Alsbrook, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-783 CIP1
; CURRENT APPLICATION NUMBER: US/10/174,333
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/193,664
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/194,614
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,063
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,066
; PRIOR FILING DATE: 2000-04-06
```

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; PRIOR APPLICATION NUMBER: 60/195,067
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,068
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; PRIOR FILING DATE: 2000-07-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 75
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-333-75

Query Match      20.1%; Score 850; DB 15; Length 694;
Best Local Similarity 30.0%; Pred. No. 2.3e-53;
Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

QY 27 NEEGSHPSNQOQTAAQENKEEKSLSKTSPTVISEPHTNIQDKLSKNSGDLTTNP 86
DB 5 NTQYSHPS-----RTHLVK-----TSDRLNRAENGLSRAHSSEETS-- 43

QY 87 DPQNAAEPTGTVPEQKEMDPGKEGNSPQKPPAAVINEYADAQHLNIVKMRQRTALY 146
DB 44 ---SVLQPG-GLAMETGLADSGGSGFTGQ-----GIARLSRLIFLLRWAARH 87

QY 147 KKKLVEGDLSSP-----BASPTAKPTAVPPVKESDDKPTHEYRLLLFKVKKML 197
DB 88 VHHQDQCPDSPDFRFRGAELKEVSSQESNAQNVGQEPADRG-----RSAW-----EL 136

QY 198 -----TEVLKRIKLPNST-DSYTDRLYLLMLLTAVLNWNCWFPIRLRVPPYQT 246
DB 137 AKCNTWTSNNTBEEKTKKDAIDVDPNSNLYRWLTALPVPFYNYLLICRACDFELQ 196

QY 247 ADNIHWLIADIICDIYLYDMLFIQRLQFVRGGDIIVDSNELRKHYRTSTKFLQDVAS 306
DB 197 SEYLMWLVLDYSADVLYLVDLV-VRATGFLQGLMVSDTNRLWQHXYKTTQFKLDVLS 255

QY 307 IIPFDICYLFFGPN-PMFRANRMLKYSFPFNFHLESDMKAYIYRVIRTTGTYLLFILH 365
DB 256 LVPTDLAYLKVGNTYPEVRFNRLKFSRLFFPDRTETRTNYPNMPFRIGNLVLYILIIH 315

QY 366 INACVYVWASNYEGIGTTRWYDG-----EGNEYLRCYVWAVRTLITIGLPEPQTL 417
DB 316 WNACIYFAISKFTIGFTGDSWVYPNISIPHEGRLSRKIYISLYWSTLTLTIGETPPVKD 375

QY 418 FEIVFOLLNFFSGVFFSSLIQOMRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLQVK 477
DB 376 EEVLVVVDVLGVLFATIVGNVGSWISNMNASRAEFQAKIDSIKQYMQFRKVTQDLET 435

QY 478 RVRTVEYTWDSORMLDESLLKTLPTTVOLALAIQVNFYSISKVDLPKGCDDTQMTYDML 537
DB 436 RVIRWFDYLVWANKKTVDEKVELKSLPDKABIAINVHLDTLKKVRIQDCEAGLVELV 495

QY 538 LRLKSVLYLPGDPVCKKGETGKEMYYIIKHGEVOVLGGPDGTVLVTLKAGSVFGEISLA 597
DB 496 LKLRPTVFGDGIYCKKGGIGKEMYYIINEGKJAV-ADGVTQFVVLSDGSYFGEISILN 554

QY 598 AGG---GNRRTANVVAHFANLITLDKTKTLEIQLVHPDSEIRILMKAR-VLLKQK---A 650
DB 555 IKGSKSGNRRTANIRSIGYSDLFCLSKDDLMALTEYPEAKKALEEKGRIILMKDNLIDE 614

QY 651 KTAETAPPRKDALALLFPPEKETPKLFTLLGGTGKASLARLL-----KLKREQAAQK 702
DB 615 ELARAGADPKDL-----BEKVQLGSSL--DTLQTRFARLLAEYNATQMKMKQRUSQUE 666
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QY 703 KENSEGGBE---EGKENEDKOKENEDKQK 728
DB 667 SQVKGGBKPLADGEVPGDATK-TEDKQK 694

RESULT 9
US-10-029-677-16
; Sequence 16, Application US/10029677
; Publication No. US20030096249A1
; GENERAL INFORMATION:
; APPLICANT: Westphal, Ryan S.
; APPLICANT: Feder, John N.
; APPLICANT: Ramanathan, Chandra S.
; APPLICANT: Mintier, Gabriel A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND POLYPEPTIDES FOR A HUMAN CATION CHANNEL
; TITLE OF INVENTION: POLYPEPTIDE
; FILE REFERENCE: D0187NP
; CURRENT APPLICATION NUMBER: US/10/029,677
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/257,865
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-029-677-16

Query Match      19.6%; Score 829; DB 14; Length 663;
Best Local Similarity 29.9%; Pred. No. 7.3e-52;
Matches 218; Conservative 132; Mismatches 283; Indels 96; Gaps 20;

QY 50 EKSLKTSPTVISEPHTNIQDKLSKNSGDLTTNPQNA--EPTGTVPEQKEMDPG 107
DB 3 EKANGVKSPPANNHHPAIPAISKGD---DHRASSRPQSAADUTSSELQOLAEMDAP 59

QY 108 KEGNSPQKPPAAVINEYA-----DAQHLNIVKMRQRTALYKKLVEGDLSSPEA 160
DB 60 QQERGFRRIARLVGLVREWAVNFRFEEPRDPSFLERFR-----GPEL 103

QY 161 SPQAKPTAVPPVKESDDKPTHEYRLLLFKVKKMLPTEYLKRIKLPNSIDSYTDRLYLL 220
DB 104 HTVTTQQGDKGDKDQEGGKTKKPELF-----VLDPAGD-WYR 142

QY 221 WLLLVTL--AYNWCWFPIRLRVPEVPTADNIHWLIADIICDIYLYDMLFIQRLQFV 278
DB 143 WLFLIALPVLVNW-CULV-ARACFSDQKGYIYVWLVDYVSDVVIAD-LFIRLTGFL 199

QY 279 RGGDIIVDSNELRKHYRTSTKFLQDVASIIPFDICYLFFGF-NPMFRANRMLKYSFPF 337
DB 200 EQGLLVKDTKKLRDNYVHTMQFKLDVASIIPTDLIYFAVGIHNPEVRFNRLHFARMFEF 259

QY 338 NHHLSIMDKAVIYRVIRTTGTYLLFILHINACVYVWASNYEGIGTTRWY----DGE--- 390
DB 260 FORTETRTSYNIFRISNLILYIIIIHWNACIYAIKSGISGFGVDVTPYNTIDPEYGY 319

QY 391 -GNEYLRCYVWAVRTLITIGLPEPQTLFEIVFOLLNFFSGVFFSSLIQOMRDVIGAAT 449
DB 320 LSREYICYLYWSTLTLTIGETPPPVKDBEYLFVIFDLIGVLFIATIVGNVGSMLSNWN 379

QY 450 ANQNTFRACMDDTIAYMNNYSIPKLQVKRVRTWYEYTWDSQRMLESDDLKTLPTTVQLA 509
DB 380 ATAEFAQIDAVKHYMQFRKVKEMEAKVIRWFDYLTWNTKKSVDERVLKKNLPAKLRAE 439

QY 510 LAIDVNFYSISKVDLPKGCDDTQMTYDMLRLKSVLYLPGDFVCKKGEIKEMYYIIKHGEV 569
DB 440 IAINVHLSTLKKVRIQDCEAGLVELVLTARPQVSPGDIYCRKGDIGKEMYYIIKEGKL 499

QY 570 QVLGGPDGTVLVTLKAGSVFGEISLLAAG--GNRRTANVVAHFANLITLDKTKTLOE 626
DB 500 AVV-ADGVTQYALLSAGSCFGEISILNIKSGKGNRTANIRSLGYSDLFCLSKDDLM 558
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QY 391 -GNEYLRCCYVAWRTLITIGGLPEQTLFEIYVQOLLNFFSGVVFSSLIGQMRDVGAA 449
Db 320 LAREYICLYWSTLTLTTIGTPPPVKBDEYLFVDFLIGVLIFATIVGNVGSIMSNW 379
QY 450 ANQNTFRACWDDTIAWMNYSIPKLVQKRVRTWYETWDSQRMDESDLLKTLPTTVQLA 509
Db 380 ATRAEQAKIDAVKHYMQFRKYSKMEAKVIRWFDVLTWTKTVDEREILKNLPAKLRAE 439
QY 510 LAIDVNFISIISKVDLPFGCDTOMYDMLRLKSVLYLPDGFVKCKGEBIKEMYIIKHGEV 569
Db 440 IATNVHLSTLKKVRIEHDCEAGLLVELKLRPQVSPGDIYCRKGDIGKEMYIIKEGKL 499
QY 570 QVLGGPDGTVLVTLKAGSVGEISLAAG--GNRRTANVAHGAFANLLTLDKKTLOE 626
Db 500 AVV-ADGGVTQVALLSAGSCFGGEISILNIGKSMGNRRRTANIRSLGSLDFCLSKDDLM 558
QY 627 ILVHPDSEIRILMKARVLLKQAKTAE---ATPPRKDLALLFPKKEETPKFKTLTGGT 683
Db 559 AVTEYFDKAKVLEERGRELIMKEGLLDENEVATSMEDVDQVKLGQLETTNMETLYTRFG-- 616
QY 684 GKASLARLLKREQAQKENSEGEGEEBEGKENEDKQEN--BDKOKENEDKGENED--- 739
Db 617 -----RLI-----AETGAQOKLKQRTVLTETKMKQ-----NEDDY 648
QY 740 -KDKGREPEKPLDRP 754
Db 649 LSDGMNSPELAAADEP 664

RESULT 12
US-09-842-758-73
; Sequence 73, Application US/09842758
; Publication No. US20030083244A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Fernandes, Blma R
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shimkets, Richard A
; APPLICANT: Malayankar, Uriel M
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E
; APPLICANT: Gangolli, Bsha A
; APPLICANT: Smithson, Glenda
; APPLICANT: Rastelli, Luca
; APPLICANT: Macdougall, John R
; APPLICANT: Taupier, Raymond J
; APPLICANT: Grosse, William M
; APPLICANT: Edward, Szekeres S
; APPLICANT: Alsobrook II, John P
; TITLE OF INVENTION: No. US20030083244A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-783
; CURRENT APPLICATION NUMBER: US/09/842,758
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/200,158
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/200,613
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,780
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/201,006
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,007
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,236
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,238
; PRIOR FILING DATE: 2000-05-01
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; PRIOR APPLICATION NUMBER: 60/201,186
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,474
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/201,508
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/220,591
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/232,678
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/263,217
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/265,160
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
; US-09-842-758-73

Query Match 19.4%; Score 820; DB 10; Length 732;
Best Local Similarity 28.8%; Pred. No. 3.8e-51;
Matches 222; Conservative 132; Mismatches 306; Indels 112; Gaps 21;

QY 24 SRNEEGSHPSNQSOQTTAQENKGE-----EKSLTKYSTPTVSEEPHTNIQ 70
Db 32 YKRWSSGKGTQMSTQCEIFRRRAQTFCESGTGHTWRMTEKSNGVKSSPANN--HNNHV 88
QY 71 DKLSKNSGDLTTNPDQNAABPTGTVPEQK--EMDPKSGPNPQNPAPVINEYA 128
Db 89 PATIKANGKDESRTSRPQSAADDDTSELQRLAEMDAPQQRGGFRFRIVLVGVIQWA 148
QY 129 -----DAQLHNLVKRMQRTALYKKLVGBDLSSEASPOKAPTAPVPKESDDKPT 181
Db 149 NNFREBEARPSFLERFR-----GPELQTVTTQOGDKGDKDGKGT 192
QY 182 EHYRLLNFKVKMKPLTEYLKILPNSIDSYDRLYLMLLLVTL--AYNNNCWFPIUR 239
Db 193 KKKFELF-----VLDPAGD--WYRWLFVIAMPVLYNN--CLLV-AR 229
QY 240 LVFPYQTDADNIHWLIADIICDIIVLYDMLFIQPLQFVRGGDIIIVDSNELKHYRTSK 299
Db 230 ACFSDLQRGYFLVWLVDYFSDVVYIAD-LFIRLRTGLEQGLLVKDPKKLRDNYIHTIQ 288
QY 300 FOLDVASIIPEDICVYLFGEF-NPMFRANRMLKYTSFFEPNHHLESIMDKAYIRVIRTTG 358
Db 289 FKLDVASIIPDIIYFVAVGIHNPFLRNLHFAFMFEFFDRTEFTSYNIFRISNLVL 348
QY 359 YLLFIILHINACVYVWASNYEGIGTTRWVY-----DGE-----GNEYLRCCYVAWRTLITIG 410
Db 349 YILVLIHWNACIYAIKSGISGFGVDTWVYPNITDPEYGLAREYIYCLYVWSTLTLTIGE 408
QY 411 LPEQTLFPIVQLNFFSGVVFSSLIQMRDVIQATANQNYFRACWDDTIAYNNYS 470
Db 409 TPPPVKDEYLEVIFDFLIGVLIFATIVGNVGSIMSNMNAEFOAKIDAVKHYMQFRK 468
QY 471 IPKLQKRVRTWYETWDSQRMDESDLLKTLPTTVQALALADVNFISIISKVDLPFGCDT 530
Db 469 VSKEMEAKVIRWFDVLTWTKTVDEREILKNLPAKLRAEIANVHLSTLKKVRIQFQCEA 528
QY 531 QMIYDMLRLKSVLYLPDGFVKCKGEBIKEMYIIKHGEVQVLGGPDGTVLVTLKAGSVF 590
Db 529 GLLVVLVLRPQVSPGDIYCRKGDIGKEMYIIKEGKLAVV-ADGGVTQVALLSAGSCF 587
QY 591 GEISLLAAG--GNRRTANVAHGAFANLLTLDKKTLOELVHPDSEIRILMKARVLLK 647
Db 588 GEISILNIGKSMGNRRRTANIRSLGSLDFCLSKDDLMETLYTRFG--NEDDY 647
QY 648 OKAKTAE---ATPPRKDLALLFPKKEETPKFKTLTGGTGKASLARLLKREQAQKKE 704
Db 648 KEGLLDENEVAASMEVDVQVKLGQLETTNMETLYTRFG-----RLI----- 687
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QY 705 NSEGEEREGKEDKOKEN--EDKOKENEDKGENEDKDKGREPEKPLDRP 754
Db 688 ----AETGAAQOKLQKORITVLEVMKQNT-----DDYLSGDMNSPEPAAAEQ 732

RESULT 13
US-10-029-677-15
; Sequence 15, Application US/10029677
; Publication No. US20030096249A1
; GENERAL INFORMATION:
; APPLICANT: Westphal, Ryan S.
; APPLICANT: Feder, John N.
; APPLICANT: Ramanathan, Chandra S.
; APPLICANT: Mintier, Gabriel A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND POLYPEPTIDES FOR A HUMAN CATION CHANNEL
; FILE REFERENCE: D0187NP
; CURRENT APPLICATION NUMBER: US/10/029,677
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/257,865
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-029-677-15

Query Match 19.4%; Score 820; DB 14; Length 732;
Best Local Similarity 28.8%; Pred. No. 3.8e-51;
Matches 222; Conservative 132; Mismatches 306; Indels 112; Gaps 21;

QY 24 SRNEEGSHPSNQSOITAEENKGE-----EKSLTKSTPTVSEEPHTNIQ 70
Db 32 TKRKWSSGKTPQWOSTCETTRRAQTCESTGHTWMTKSNVGVKSPANN---HNNHV 88
QY 71 DLSKQSSGDLTNPDPQNAEPTGTVPQK--EMDPGKEGPNSPKNPPAAPVINEYA 128
Db 89 PATIKANGKDSRTSRPQSAADDDTSELQLAEMDAPQRRGGRFRIVLGVIRQWA 148
QY 129 -----DAQHLNLVKNRQRTALYKKLVBGDLSSPEASPTAKTAVPVKSGSDKPT 181
Db 149 NRNFREEARPSFLERFR-----GPELQTVTVOQDGKDGKDGKGT 192
QY 182 EHYVRLWFKYKMWPLTYLXKILPNSIDSYTDELILLMLLVTL--AYNWCWFILR 239
Db 193 KKKFELF-----VLDPAGD--WYRMLFVAMPVLYNM--CLLV-AR 229
QY 240 LVFPYQADNIHYWLIADIIIDYVDMLEFIQPRLOFVRGDDIIVDSNELRKHVTSK 299
Db 230 ACFSDLQRYGLVWLVLDYFSDVVIAD-LFIRLTGFEQGLLVKDPKLRDNYHTLQ 288
QY 300 FOLDVASIIPDICYLPFGP--NPMFRANRMLKYTFPEFNHLSIMDKAYIYRVIRTTG 358
Db 289 FKLDVASIIPDTLIVFAVGIIHNPFLRNLLHFARMFEFDTTETRTSYNPIFRISNLVL 348
QY 359 YLLFILHINACVYVWASVEGIGTRWY-----DGE-----GNEVLRVYVAVRLITIGG 410
Db 349 YILVLIHWNACIYVAISKISGFGVDVTWYPTNITDPEYGLAREYIYCLYNSTLTLTIGE 408
QY 411 LPEQTLFEIVFOLLNFPSSGVVFSLLIGOMRDVIGATANQNVFRACMDDTIAYMNNYS 470
Db 409 TPPPVKEEYLVFVDFELIGVLITATIVGVNVSISNNATRAEFQAKIDAVKHYMQPRK 468
QY 471 IPKLVRKRVRTWYBYTWDQSRMLDESLLKTLPTTQVLAIDVNFISIISKVDLFKGCOT 530
Db 469 VSKEMEAVKIWPDLWNTKNTVDREVLKPLAKRAEIAINVHLSTLKKVRFQDCEA 528
QY 531 QMIYDMLRLKSVLYLPDGFVKCKGETGKEMWIIKHGEVQVLGGPDGTHKVLVLKAGVP 590
Db 529 GLLVELVLKLRPQVFSFGDYGCRKGDIGKEMYIIKEGLAVV-ADDOGVTOVALLSAGSCF 587
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QY 591 GEISILAAAGG---GNRRTANVVAHGFANLLTLDKKTLQELVHYDPDSERILMKKARVLK 647
Db 588 GEISILNITKSGKGNRRTANIRSLGYSDLFCLSKDDLMEAVTEYDPAKKVLEERGRELIM 647
QY 648 QKAKTAE---ATPPRKDLALLFPKPEETPKLFTKLLGGTGKASLARLLKLKREQAQKKE 704
Db 648 KEGLLDENEVAASMEVDVQEKLKQLETNNMETLYTRFG-----RLL----- 687
QY 705 NSEGEEREGKEDKOKEN--EDKOKENEDKGENEDKDKGREPEKPLDRP 754
Db 688 ----AETGAAQOKLQKORITVLEVMKQNT-----DDYLSGDMNSPEPAAAEQ 732
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RESULT 14
US-10-174-333-73
; Sequence 73, Application US/10174333
; Publication No. US20040029220A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Smithson, Glenna
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Grosse, William M.
; APPLICANT: Szekeres, Edward S.
; APPLICANT: Alsobrook, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-783 CIP1
; CURRENT APPLICATION NUMBER: US/10/174,333
; CURRENT FILING DATE: 2002-06-18
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/193,664
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/194,614
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,063
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,066
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,067
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,068
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; PRIOR FILING DATE: 2000-07-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: Curoseqlist version 0.1
; SEQ ID NO 73
; LENGTH: 732
; TYPE: PRT
```

```
; ORGANISM: Oryctolagus cuniculus
US-10-174-333-73

Query Match      19.4%; Score 820; DB 15; Length 732;
Best Local Similarity 28.8%; Pred. No. 3.8e-51;
Matches 222; Conservative 132; Mismatches 306; Indels 112; Gaps 21;

Qy 24 SRNREGSHPSNQSOQTQAENKGE-----EKSLTKSTPVTSEBPHNIQ 70
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 32 TKRWSSGKTPQSTOCETERRAQPCSTGHTWMTKASNGVKSPPANN---HNNHV 88
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 71 DLSKSNSSGDLTTPNPQNAAEPTGTVPQK--EMDPGKSGPNSPQKPPAAPVINEYA 128
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 89 PATIKANGKDSRSTRSPQSAADDDTSSELQRLAEMDAPQRRGFRIVLVGVIRQWA 148
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 129 -----DAQLHNLVKMRQRTALYKKLVKGLVEGDLSSPEASPTAKTAVPPVKESDDKPT 181
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 149 NRNPREBEARSDSFLERFR-----GPELQVTVTQOGDKGDKGDKGKT 192
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 182 EHYRLLWFKVKMPLTEYLKRIKLPNSIDSYTDRLYLLMLLVTL--AYNWNCFPIPLR 239
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 193 KKKFELF-----VLDPAGD--WYRWMLFVIAMPVLYNW-CLLV-AR 229
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 240 LVFPYQFADNIHYWLIADIICDIILYDMLPIQPRLOFVRGGDIIVDSNELKHYRTSTK 299
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 230 ACFSDLQRGYPLWLVLDYFSDVVIAD-LFIRLRTGFLQGLLVKDPKKLRDNYIHTLQ 288
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 300 FOLDVASIIPDICYLPFGF-NPMFRANMLKYTSFEFNHLESIMDKAYIYRVRTTG 358
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 289 FKLDDVASIIPDIIYFAVGHINPELRNLLHFARMFEFDRTERTSYNIFRISNLVL 348
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 359 YLLFILHINACVYVWASNYEGIGTRWVY-----DGE-----GNEYLRCYVAVRTLTIGG 410
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 349 YILVIHWNACIYVIAISKSIGFGVDVTWYVNIPTDEYGLAREVIYCLYVSTLTITIGE 408
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 411 LPEPQTLFEIVFQLLNPFSGVFPSSLIQMRDVGIGAAATANQNYFRACMDDTIAYMNNYS 470
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 409 TTPPVKDEEYLFVIFDFLIGVLIPATIVGNVGMISNMNATRAEFQAKIDAVKHYMQFRK 468
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 471 IPKLQVRKVRTWYETWDSQRMDESLLKTLPTTVQLALADVNFESIISKVDLPKGCOT 530
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 469 VSKEMEAKVKNFDYLTWNTKKTVDEREVLNKLPAKRAETAINVHSTLTKKRFIDQCEA 528
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 531 QMIYDMLRLKSLVLYLPDGFVCKKGEIKGEMYIIKHGEVQVLGPGDPTKVLVTLKAGSVF 590
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 529 GLLVELVLKLRPQVSPFSGDYICRKGDIKGEMYIIKEGKLAVV-ADDGVTQYALLSAGSCT 587
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 591 GEISLLAAGG---GNRRTANVAVGFANLLTLQKTLQELVHPDSEIRILMKKARVLK 647
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 588 GEISILNIGSKMGNRRTANIRSLGYSDLFCLSKDDLMEAVTEYDPAKKVLEERGRIILM 647
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 648 QKAKTAE---ATPPRKDLALLFPPEETPKLFTKLTLMETLYTRFG-----RLL----- 687
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 705 NSBGBEEGKKNEDKOKEN--EDKOKENEDKGENEDKKGREPEPKPLDRP 754
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 688 ----AETGAQOKLQKRIITVLEVKMKQNTB---DDYLSLSDGMNSPEPAAAEQ 732
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
US-09-735-927-2
; Sequence 2, Application US/09735927
; Patent No. US20020137128A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000834
; CURRENT APPLICATION NUMBER: US/09/735,927
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 60/231,570
```

```
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 664
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-735-927-2

Query Match      19.4%; Score 819.5; DB 9; Length 664;
Best Local Similarity 29.5%; Pred. No. 3.6e-51;
Matches 217; Conservative 129; Mismatches 285; Indels 105; Gaps 21;

Qy 50 EKSLTKSTPVTSEBPHNIQDKLSKSNSSGDLTTPNPQNAAEPTGTVPQK--EMDPG 107
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 3 EKTNGVKSPANNHHA---PPAIKANGKDDHRTSSRPHSAADDDTSSELQRLAEDVAP 59
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 108 KEGPNSPQKPPAAPVINEYADAQLH-----NLVKMRQRTALYKKLVKGLVEGDLSSPEA 160
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 60 QQGRSGFRIRIVLVGIIREWANKNFRPEPRDPSFLERF-----GPEL 103
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 161 SPQTAKPTAVPPVKESDDKPTTEHYRLLWFKVKMPLTEYLKRIKLPNSIDSYTDRLYLL 220
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 104 QVTVTQEGDKGDKGDKGDKTKKKELF-----VLDPAGD--WYTC 142
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 221 WLLLVTL--AYNWNCFPIPLRVFPYQFADNIHYWLIADIICDIILYDMLPIQPRLOFV 278
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 143 WLFVIAMPVLYNW-CLLV-ARACFSDLQGYVLYWLVLDYFSDVVIAD-LFIRLRTGEL 199
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 279 RGGDIIVDSNELKHYRTSTKFLQDVASIIIPDICYLPFGF-NPMFRANMLKYTSFEFF 337
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 200 EQGLLVKDTKLRDNYIHTLQFKLDVASIIPDIIYFAVGHINPELRNLLHFARMFEF 259
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 338 NHLESIMDKAYIYRVRTTGILLFILHINACVYVWASNYEGIGTRWVY-----DGE--- 390
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 260 FDRTERTSYNIFRISNLVLIHWNACIYVIAISKSIGFGVDVTWYVNIPTDEYGY 319
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 391 -GNEYLRCYVAVRTLTITIGLPEPQTLFEIVFQLLNPFSGVFPSSLIQMRDVGIGAA 449
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 320 LAREVIYCLYVSTLTITIGETPPVKDEEYLFVIFDFLIGVLIPATIVGNVGMISNMN 379
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 450 ANQNYFRACMDDTIAYMNNYSIPKLQVRKVRTWYETWDSQRMDESLLKTLPTTVQLA 509
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 380 ATRAEFQAKIDAVKHYMQPRKVSKGMEAKVIRWFDYLTWNTKKTVDEREVLNKLPAK 439
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 510 LAIDVNFESIISKVDLPKGCOTQMIYDMLRLKSLVLYLPDGFVCKKGEIKGEMYIIKH 569
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 440 IAINVHSTLTKKRFIDQCEAGLLVELVLKLRPQVSPGDIYICRKGDIKGEMYIIKEG 499
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 570 QVLGPGDPTKVLVTLKAGSVFGEISLLAAGG---GNRRTANVAVGFANLLTLDKKTLQ 626
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 500 AVV-ADDGVTQYALLSAGSCTFGEISILNIGSKMGNRRTANIRSLGYSDLFCLSKD 558
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 627 ILVHPDSEIRILMKKARVLKQKAKTAE---ATPPRKDLALLFPPEETPKLFTKLT 683
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 559 AVTEYDPAKKVLEERGRIILMKKEGLLDENEVATSMEDVQEKLGQELTNMETLYTRFG-- 616
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 684 GKASLARLLKLRQEAQAKKENSEGEEGKKNEDKOKEN--EDKOKENEDKGENED-- 739
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 617 -----RLL-----AETGAQOKLQKRIITVLETKOKQN-----NEDDY 648
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 740 -KDKGREPEPKPLDRP 754
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 649 LSDGMNSPELAAAEF 664
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Search completed: March 27, 2005, 21:27:19
Job time : 1174 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 27, 2005, 20:25:22 ; Search time 51 Seconds  
(without alignments)  
1526.262 Million cell updates/sec

Title: US-09-855-828-1  
Perfect score: 4234  
Sequence: 1 MFKSLTKVKNVKPIGENNEN.....PSABGGBEVLTVIEVKEKAKQ 809

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1952	46.1	909	2 S32538	cGMP-gated cation
2	1095	25.9	800	2 T19627	hypothetical prote
3	834.5	19.7	695	2 S74179	cyclic nucleotide-
4	829	19.6	663	2 S11521	cAMP-gated channel
5	821.5	19.4	735	2 I50630	alpha subunit of c
6	820	19.4	732	2 S35691	cyclic nucleotide-
7	819.5	19.4	688	2 B42161	cGMP-gated cation
8	818.5	19.3	690	2 A42161	cGMP-gated cation
9	818	19.3	686	1 A4842	cGMP-gated ion cha
10	807.5	19.1	682	1 JH0560	cyclic nucleotide-
11	804	19.0	664	2 S11517	cyclic nucleotide-
12	801.5	18.9	691	2 J66509	rod cyclic nucleot
13	797	18.8	690	1 S07103	cGMP-gated ion cha
14	794	18.8	706	2 A5251	cyclic nucleotide-
15	771	18.2	645	2 I50680	alpha subunit of r
16	770	18.2	772	2 S28292	hypothetical prote
17	718	17.0	665	2 S52072	DmGNC protein - f
18	640	15.1	575	2 I59327	olfactory cyclic n
19	555	13.1	673	2 T20936	hypothetical prote
20	530	12.5	611	2 T20935	hypothetical prote
21	484	11.4	261	2 I78559	cyclic nucleotide-
22	476	11.2	261	2 I78560	cyclic nucleotide-
23	441.5	10.4	644	2 T33125	hypothetical prote
24	366.5	8.7	767	2 T21969	hypothetical prote
25	349	8.2	828	2 T52045	potassium channel
26	349	8.2	962	2 I53197	potassium channel
27	336	7.9	989	2 I48912	potassium channel
28	331.5	7.8	807	2 T12177	potassium channel
29	323.5	7.6	845	2 T07052	probable potassium

30	321	7.6	688	2 S55349	potassium channel
31	318	7.5	787	2 S68699	potassium channel
32	317.5	7.5	1159	2 I38465	probable potassium
33	314	7.4	883	2 T07651	potassium channel
34	313.5	7.4	662	2 T04461	potassium channel
35	311	7.3	887	2 T03939	potassium channel
36	302.5	7.1	838	2 S23606	potassium channel
37	302.5	7.1	857	2 S62694	potassium channel
38	296	7.0	934	2 T42394	potassium channel
39	292	6.9	1174	2 A40853	potassium channel
40	287	6.8	716	2 T51354	cyclic nucleotide-
41	284	6.7	706	2 T51432	cyclic nucleotide-
42	282	6.7	880	2 F85381	potassium channel-
43	282	6.7	916	2 T05360	probable potassium
44	280	6.6	702	2 T04424	probable calmoduli
45	278.5	6.6	718	2 G84902	hypothetical prote

ALIGNMENTS

RESULT 1

S32538  
cGMP-gated cation channel 2, rod - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 17-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S32538  
R:Chen, T.Y.; Peng, Y.W.; Dhallan, R.S.; Ahamed, B.; Reed, R.R.; Yau, K.W.  
Nature 362, 764-767, 1993  
A:Title: A new subunit of the cyclic nucleotide-gated cation channel in retinal rods.  
A:Reference number: S32538; MUID:93226050; PMID:7682292  
A:Accession: S32538  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-909 <CHE>  
A:Cross-references: UNIPROT:O43636  
C:Keywords: cGMP binding  
F:620-742/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 46.1%; Score 1952; DB 2; Length 909;

Best Local Similarity 46.4%; Pred. No. 2.9e-112; Indels 110; Gaps 18;  
Matches 405; Conservative 121; Mismatches 237;

Qy	14	IGENNEEQSRNEEGSHPSNQQTAAQ--ENKGE---EKLTKTKSTVTSEPTN 68
Db	67	VGEAAKKEAEKAEAEAEVAEEAEKQDWAETKEEPEAEAEAAAGVGVPATKQHPVQ 126
Qy	69	IQDK-----LSKNSSGDLTTNPDPQNAAEPTGTVPQKEMDPGKEGN----- 112
Db	127	VEDTDADSCPLMAEENPPS--TVLPFSPAKSDTLIVPSSASGTHRKKLPSEDEAEELK 184
Qy	113	--SPQNKP-----PAAP-----VINEYADAQLHNLVKRMORTALY 146
Db	185	ALSPAESPVVAMSDPTPKDTGDQDRAASTASTNSALIND----RLQELVKLFKERTKV 240
Qy	147	KKKLVEGDLS----SPEASQTAKTAPVVPKESDDKPT--EHYVRLLMFKVKMPLTEY 200
Db	241	KEKLIDPVTSDSESPKPAKAPADPTKPAEAPVEEHEHYCDMLCCFKHPRWKY 300
Qy	201	LKR1KLPNSIDSYDRLLYLLVLLVLAANNWCNFIPLRLVFPYQTDADNIHWLIADIC 260
Db	301	---QFQSIDPLTNLMYVLMVFFVMAWNNWNCWLIIPVRWAFPYQTDPNIHLLMDYLC 356
Qy	261	DIILYDMLFQPLQVRGDIIVDSNELRKHRTSTKFGVLVASIIPFCIVLFGFN 320
Db	357	DLIYFLDITVFQTLQVFRGDIITDKDMNNYKRRFKMDLLSLPLDFLYLKGVN 416
Qy	321	PMFRANMLKYSFFEFNHLESIMDKAYIVRVITRTGYLILFILHINACVYVWASNEGI 380
Db	417	PLLRPLCKLYMAFEFNSRLSILSKAYVRVITRTAYLLYSLHNSCLYVWASAYQL 476
Qy	381	GTTRWVYDGEENYLCRYNAVRTLITIGGLPEPQTLEIVFQQLNFPFVSLSLIGQ 440

Db 477 GSTHWVYDGVGNSYRCYYFAVKTLTITIGLPPDKTLFIIVFOLLNYYFTGVFAFVMIQ 536

QY 441 MRDVI GAATANQNYFRACMDTITAYWNNYSIPKLVQKVTWYETWDSQRMLEDSDLLK 500

Db 537 MRDVGAATAGQTYRSCMDSTVKYWNFYKIPKSVQNRVKTWYETWHSQGLMDESELMV 596

QY 501 TLPPTVQLALAIQVNFNIIISKVDLFFKQCDQMTIYDMLLRKLSVLYLPQDFVCKKGBIGKE 560

Db 597 QLPDKWRLDLAIQVNVIVSKVALFQCDQMTIYDMLLRKLSVLYLPQDFVCKKGBIGRE 656

QY 561 MYIIKHGEVOLGPDGDKVLTWKAGSVFGEISLAAAGGNRRRTANVAHGFANLLTLD 620

Db 657 MYIIQAGVQVGLGPDGKSVLVTWKAGSVFGEISLAAAGGNRRRTANVAHGFANLLTLD 716

QY 621 KKTLOEILVHPDSEIRILMKARVLKQAKTAETAPPRKDLALLPPKKEETPKLFTLL 680

Db 717 KDLNEILVHPYEQKLLRKARMLRSNNK-----PKEEKSVLIIAPPRAAGTPKLFNAAL 771

QY 681 GGTGKAS-----LARLLKREQAACKENSEGEGEKENEDKQENEDKQK 728

Db 772 AMTKWGGKAGKGLAHLRLKELALEAAKQDEL---VEQAKSSQDVKGEGSAAP 828

QY 729 ENEDKQKE-NEDKDKGREPEKP-----LDRPECTASPIAVEEPHPSVRRTVLP 776

Db 829 DQHTHPKEAATDPPAPRTPEPPGSPSPASLGRPEGEERGPA-EPEHSVR-----882

QY 777 RGTSRSLIISMAPSAEGGEVLTIEVKEKAKQ 809

Db 883 -----ICMSPGPEPGEOILSVKMPEREE 906

RESULT 2

T19627

hypotheical protein F36F2.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T19627; T21863

R;Kershaw, J.

submitted to the EMBL Data Library, April 1997

A;Reference number: Z19153

A;Accession: T19627

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-800 <W12>

A;Cross-references: UNIPROT:O62237; EMBL:Z93778; PIDN:CAB07847.1; GSPDB:GN00019; CBSP:F36F2.5

A;Experimental source: clone C31H5

R;Cottage, A.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z19479

A;Accession: T21863

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-800 <W12>

A;Cross-references: EMBL:Z81532; PIDN:CAB04328.1; GSPDB:GN00019; CBSP:F36F2.5

A;Experimental source: clone F36F2

C;Genetics:

A;Gene: CBSP:F36F2.5

A;Map position: 1

A;Introns: 27/3; 51/2; 142/2; 191/3; 287/3; 333/3; 355/2; 405/1; 433/2; 484/1; 508/1; 56

Query Match 25.9%; Score 1095; DB 2; Length 800;

Best Local Similarity 31.9%; Pred. No. 1.3e-59;

Matches 258; Conservative 153; Mismatches 301; Indels 98; Gaps 22;

QY 2 FKSLSKVKVYKPTIGENNENQSGRRNEEG---SHPNQSQOQTTAENKGEKSLTKYST 58

Db 21 FSVVDQKASKPT-QLSEKWKSPRSDPSDLDDPANAS-----KEPSASTRPL 68

QY 59 PV-TSEPHNTIQDKLSKNSGDLTNP-----DQNAAEPTGTVPEQKEMDPGKEGN 112

Db 69 FYPPTRPPEVYQI-----DEVESPLIGLIDETDDHLDG-----RLDPAASFDA 113

QY 113 SPQNKPPAAPVINEYADAQ-----LHNLVKMRQRTALYKKLVEGLDSSPEASPT 164

Db 114 NSLSATRASSIIEDVRSQISFIMRERLHSAKEVHRRTSAVREDLIR---ETPEDTVSM 170

QY 165 AKPTAVPPVKESDDKPTHEHYLLWFKVK-KMPLTEYLKR---IKLPNSIDSYDRLYLL 220

Db 171 A--SNVP--KQNEHRPS--LMSLIGLQNRSESTVDTVKNCFGFSLKGTFFHPY-GRFYMT 223

QY 221 WLLVTLAYNMWCWFIPLRVFPYOTADNIHYWLIADIICDIIYLYDMLFIQPLQFVRG 280

Db 224 WLSLVTLCFLNAPCIPLRSSYPYQADNMWTFWIDVYSCDLVYVIDMLLIKPLRAFTRG 283

QY 281 GDIIVDSNELRKHYRTSTKQLDVAIIIPDFICYLFFGFNPMFRANRMLKYTSFFFNHH 340

Db 284 GIQVKIYKDTQRHYLMWTRFKLDLILSLPTDLMYFFGKMPIWRINRVLKINSFWLLFDM 343

QY 341 LESIMDKAIIYRVIRTTGYLLFIHLINACVYVWASNYEGIG-----TTRVVDYG 389

Db 344 LQNSFANPAIARIARTLSYMIYIIHCNSCVYKLSALQAFQIAYLENGKWYLNKWVYNN 403

QY 390 EGNELRCYVAVRVTLITIGLPEPQTLFEIVFOLLNFFSGVFFSSLIGQMRDVIQAAT 449

Db 404 QGNVIRCFYFAAATSTGNNPAPTNIYIEYIMTCSWMMGVFVPALLIGQIRDIVSNAN 463

QY 450 ANQNYFRACMDDTIAYMNNYSIPKLVQKRVTWYETWDSQRMLEDSDLLKTLPTTVQLA 509

Db 464 RNREEFORKMDLALGECKKGLKMETNTRVDFIYTWQOQKTLDEKKLIEKLPLQLTD 523

QY 510 LAIDVNFISIISKVDLPKQCDQMTIYDMLLRKLSVLYLPQDFVCKKGEIKEMVLIKHGEV 569

Db 524 LALSVDYTLTSVQLVFQDCDRALLDLVLKRPVFLPGDMICLKGVDGVKEMVIINQGL 583

QY 570 QVLGGPDGTVLTKAGSVFGEISLAAAGGNRRRTANVAHGFANLLTLDKKTLEIIV 629

Db 584 QVGGDHNEKIPAEIAQAGVFGFGEISLAAAGGNRRRTASIRAKGYCTFLVLAKEDLNDVIR 643

QY 630 HYPDSEIRILMKARVLKQAKTAETAPPRKDLALL-----PPPKEETPKLFTLLGGT- 683

Db 644 YYPQAQTLIRRKAAAMLKNDKSKDEKTEKIKQAQAELEDRCKINPR-QVPEKLTILIANMTE 702

QY 684 -----GKASLARLLKLRQAAQK-----ENSEGGEEGEKENEDKQENED-----725

Db 703 MNENKGVQELKKVIEETEKSRRQSIYYPWSTLQRRDDDEEENDEEDLSVDGEDFLDP 762

QY 726 -KQENEDKQENEDKDKGREPEEKPLDRP 754

Db 763 TNHSDDED---PMEDVDLAPEVHDDWDQF 789

RESULT 3

S74179

cyclic nucleotide-gated channel protein - human

C;Species: Homo sapiens (man)

C;Date: 14-Apr-1998 #sequence\_revision 24-Apr-1998 #text\_change 16-Jul-1999

C;Accession: S74179

R;Yu, W.P.; Grunwald, M.E.; Yau, K.W.

FEBS Lett. 393, 211-215, 1996

A;Title: Molecular cloning, functional expression and chromosomal localization of a human

A;Reference number: S74179; MUID:96409310; PMID:8814292

A;Accession: S74179

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-695 <YUM>

A;Experimental source: retina

C;Genetics:

A;Map position: 2

C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-

C;Keywords: ion channel; ion transport; membrane protein

F;482-607/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 19.7%; Score 834.5; DB 2; Length 695;

Best Local Similarity 29.7%; Pred. No. 1.2e-43;

Matches 223; Conservative 149; Mismatches 271; Indels 107; Gaps 22;







Db 3 LSMKNTIINTWHSFVNIPNVIVPAIEKEIRRMENAGACSFSDDDN-----GSLSESENE 57

Qy 106 PG-----REGPNSPQKPPAAPV---INEYADAQLHNLVKRMQRORTALYKKKLVEGD 154

Db 58 DSFFPSNSYKRGPSQREQLPGTWTALFNVNSSNKDQEPKCKKKK-----EKSKADD 113

Qy 155 LSSPASQOTAKPTAVPPVKESDDKPTTHYRLLMFKVKOMPLTYLKRKIKLPNSIDSYT 214

Db 114 KNEKKDQPEKKKKE-----KEKEKKKKE-----KTKEKEKEKEKEVWIDPSGNTYY 162

Qy 215 DRLVLLMLLVTL--AYNWCWFIPLRLVFPYQATADNIHYMLIADICDIILYLDMLFIQ 272

Db 163 N-----WLFCTLPWYNT--MIARACFDELQSDYLEWLIIFYNSNVVLADM--FVR 214

Qy 273 PRQVQRGGDIIVDSNELKRYSTKQQLDVASIIIPEDICYLFFGFN--PMFRANRMLKY 331

Db 215 TRTGLEQGLLVKDRMKLIEYKANKLQKLDVLSVITDLYIKFGWNYPEIRLNRLRI 274

Qy 332 TSFPEFNHLSIMDKAIYIRVIRTTGYLLFILHINACVYTWASNYEGIGITRWY---- 387

Db 275 SRMFEFFORTTETRTNYPNIFRISNLVMYIVIIHWNACVYISISKAIFGNDTWYYPDVN 334

Qy 388 DGE-----GNEYLRCYVAVRTLITIGLPEPQTLPEIVFQLLNFFSGVVFSSLIQMRD 443

Db 335 DPEGLRLARKVYSLSYLTLTITIGETPPVLDSEYIFVVDVLIGLIVFATIVGNIGS 394

Qy 444 VIGATANQNYFRACMDDTIAYMNNYSIPKLVQKRVRTWYETWDSQRLMDESLLKTLPL 503

Db 395 MISNNAARAEFQSRVDAIKQYMFNRVNSKDMKEVWKWFDYLTWNTKKTVDEREVLRLP 454

Qy 504 TVVQLALADVNFISIIKVDLFGKCDTQMIYDMLRLKSVLYLPGDFVCKKGEGIKENYI 563

Db 455 DKLRAEIAINVHLDTLKKRIFADCEAGLLVELVLKLPQVYSPGDYICKKGDIGREMYI 514

Qy 564 IKHGEVQVLGGPDKTKVLTAKGSVFGEISILAAAG--GNRTANVAVHGFANLLTLD 620

Db 515 IKEGKLAVV--ADDGTTQVFLSDGSYFGEISILNIGSKAGNRRTANIKSIGYSLDFCLS 573

Qy 621 KKTQELILVHPDSEIRILMKARVLL 646

Db 574 KDDLMEVLTEYPDAKTWLKEGRQIL 599

RESULT 8

A42161

cGMP-gated cation channel, rod photoreceptor - human

N:Alternate names: rod photoreceptor cGMP-gated channel

C:Species: Homo sapiens (man)

C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004

C:Accession: A42161

R:Pittler, S.J.; Lee, A.K.; Althert, M.R.; Howard, T.A.; Seldin, M.F.; Hurwitz, R.L.; Wa

J. Biol. Chem. 267, 6257-6262, 1992

A:Title: Primary structure and chromosomal localization of human and mouse rod photorece

A:Reference number: A42161; MUID:92210603; PMID:1372902

C:Accession: A42161

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-690 <P>

A:Cross-references: UNIPROT:P29973; GB:M84741; NID:g180461; PIDN:AAA52010.1; PID:g180462

A:Title: Human rod photoreceptor cGMP-gated channel; amino acid sequence, gene structure

C:Superfamily: cyclic nucleotide-gated channel; CAMP receptor protein cyclic nucleotide-

C:Keywords: cGMP binding; transmembrane protein

F:479-603/Domain: CAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 19.3%; Score 818.5; DB 2; Length 690;

Best Local Similarity 30.0%; Pred. No. 1.1e-42;

Matches 221; Conservative 128; Mismatches 262; Indels 125; Gaps 22;

Qy 5 LTKVNVKPIGENNENEGSSRRNEEGSHPS-----NQSQQTAAQENKKEE-----KSL 53

Db 17 VTMPNVIVP-----DIEKEIRRMENAGACSFSDDDSAYTSEENENPHARGSFYSKSL 71

Qy 54 KTKSTPTVTSPEPHNIQDKLSKSSGDLTTNPPQNAABTGTVPQEKMDPKGEGNS 113

Db 72 R-KGGPSQREQLFCATAIFNVNNS-----NKD-----QEPEEKKKKKKKKSKDDKNE 121

Qy 114 POKPPAPVINEYADAQLHNLVKRMQRORTALYKKKLVEGLSSPEASPOKTAQTAVPDV 173

Db 122 NKNDPE-----KKKKKKKKKK-----E 141

Qy 174 KESDDKPTHEHYRLLMFKVKOMPLTEYLKRIKLPNSIDSYTDRLLYLLMLLVTL--AYNW 231

Db 142 EKSKDKKEHH-----KKEVVV-----IDP-SGNTYNNWLCITLTPVMYNW 180

Qy 232 NCWFIPLRLVFPYQATADNIHYMLIADICDIILYLDMLFIQPRLOQVVRGGDIIVDSNELR 291

Db 181 T--MVIARACFDELQSDYLEWLIIFYNSNVVLADM--FVRIRTYGLSQGLLVKELKLI 237

Qy 292 KHYRTSTKQQLDVASIIIPEDICYLFFGFN--PMFRANRMLKYTSFPEFNHLSIMDKAYI 350

Db 238 NKYSKNLQKLDVLSIPTDLYIKFGWNYPEIRLNRLRFSRMFEFFORTTETRTNYPN 297

Qy 351 YRVIRTTGYLLFILHINACVYTWASNYEGIGITRWY----DGE-----GNEYLRCYVAV 402

Db 298 FRISNLVMYIVIIHWNACVYISISKAIFGNDTWYYPDVINDPEFGLRLARKYVYSLYWS 357

Qy 403 RLTITIGLPEPQTLPEIVFQLLNFFSGVVFSSLIQMRDVIAGATANQNYFRACMDDT 462

Db 358 LTLTIGETPPVLDSEYIFVVDVLIGLIVFATIVGNIGSMISNNAARAEFQARIDAI 417

Qy 463 IAYMNNYSIPKLVQKRVRTWYETWDSQRLMDESLLKTLPTTVQLALADVNFISIIISKV 522

Db 418 KQYMFNRVNSKDMKEVWKWFDYLTWNTKKTVDKEVLYLPGDKLRAEIAINVHLDTLAKV 477

Qy 523 DLFGKCDTQMIYDMLRLKSVLYLPGDFVCKKGEGIKENYI IKHGEVQVLGGPDKTKVLT 582

Db 478 RIFADCEAGLLVELVLKLPQVYSPGDYICKKGDIGREMYI IKEGKLAVV--ADDGTTQV 536

Qy 583 TLKAGSVFGEISILAAAG--GNRTANVAVHGFANLLTLDKKTLOETLVHVPDSEIRILM 639

Db 537 VLSGDTFGEISILNIGSKAGNRRTANIKSIGYSDLPCLSKDDLMELALTEYPDAKTWLE 596

Qy 640 KKAARVLLKQKA---KTAEATPPKDLALLPPPKKEETPKLPKTLIGGTGKASLARLL--- 692

Db 597 EKGQILMKDGLLDLNIANAGSDPKDLKEEKVTRMEGSDVLAQT-----RPARILAEY 648

Qy 693 -----KUKREQAOKK 703

Db 649 ESMQQLKQRLTKVEK 664

RESULT 9

A44842

cGMP-gated ion channel protein - human

N:Alternate names: rod photoreceptor cGMP-gated channel

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: A44842

R:Dhallan, R.S.; Macke, J.P.; Eddy, R.L.; Shows, T.B.; Reed, R.R.; Yau, K.W.; Nathans, J.

J. Neurosci. 12, 3248-3256, 1992

A:Title: Human rod photoreceptor cGMP-gated channel: amino acid sequence, gene structure

A:Reference number: A44842; MUID:92356211; PMID:1379636

A:Accession: A44842

A:Molecule type: mRNA

A:Residues: 1-686 <DHA>

A:Cross-references: GB:S42457; NID:g252853; PIDN:AAB22778.1; PID:g252854

A:Experimental source: retina

A>Note: sequence extracted from NCBI backbone (NCBIN:110250, NCBI:P.110251)

A>Note: intron positions were determined from genomic sequence

C:Genetics: CNCG

A:Gene: GDB:CNCG1; OMIM:123825

A:Cross-references: GDB:127557; OMIM:123825

A:Map position: 4p14-q43

A:Introns: 36/2; 75/2; 95/2; 110/2; 146/2; 182/2; 218/2

C:Superfamily: cyclic nucleotide-gated channel; CAMP receptor protein cyclic nucleotide-

C:Keywords: cGMP binding; eye; ion channel; ion transport; retina; transmembrane protein

F:475-599/Domain: CAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match		19.3%; Score 818; DB 1; Length 686;
Best Local Similarity		25.9%; Pred. No. 1.2e-42;
Matches		226; Conservative 129; Mismatches 266; Indels 136; Gaps 24;
Qy	5	LTKVKKYKPTGENNENFQSRNREGSHPS-----NQSQQTAAQENKGE-----KSL 53
Db	13	VTWPNVIVP-----DIEKEIRRMENGACSFSEDDDSASTSESESENPHARGSFYSKSL 67
Qy	54	KTKSTPTVTSBEPHTNIQDKLSKNSGDLTTNPDPPNAEAPTGTVPQKMDPGKEGPN 113
Db	68	R-KGPPSQRQYLPQALAFVNNSS-----NKD-----QEPKPKKKKKKKSKDNKNE 117
Qy	114	PONKPPAAPVINEYADAQLHNLVKRMQRORTALYKKLVEGDLSSPEASPTAKPTAVPPV 173
Db	118	NKNDPE-----KXKKKKDKKKKK-----E 137
Qy	174	KESDDKTEHYRYLLWFKVKKMPLETEYLKRIKLPNSIDSYDRLYLWLLLVTL--AYNW 231
Db	138	EKSOKKKEE-----KKEVV-----IDP--SGNTYNNWLCITLPVWYNN 176
Qy	232	NCWFIPRLVFPYQTADNIHLYADIICDIILYDMLFIQPRLOFVRGGDIIVDSNELR 291
Db	177	T--WVIARACFDELSQDYLEWLLIDVSDIVLIDM-FVTRTGYLEQGLLVKEELKLI 233
Qy	292	KHYRTSTKFOLDVASIIPFDICVLPFGFN--PMFRANRMLKYTFEFNHHLESIMDKAYI 350
Db	234	NKYKSNLQFKLDVLSIPTDLLYFKLGWNYPEIRLNNLFRSFRWFPFQRTETRTNYPNI 293
Qy	351	YRVIRTTGYLLFILHINACVYVWASNYEGIGTRTWY-----DGE-----GNEYLRCYWAV 402
Db	294	FRISNLVYIVIIHWNACVYFYSISKAGFGNDTWVPYDINDPDEFGLARKYVYSLYWST 353
Qy	403	RTLITIGLPEPQTLPEIYFOLLNFPFSGVVFSSLIGOMRDVIGATANQNYFRACMDDT 462
Db	354	LTLTTIGETPPVDSYVFWVDLIGVLIFATIVNGISMLSNMNAARAEQARIDAI 413
Qy	463	IAYMNNYSIPKLQKRVRTWYETWDSORMDESLLKTLPTTVQLALAIQVNFISIISKV 522
Db	414	KQYHPRNVSKMEKRVIKFWDYLTWTKVTDEKEVLKPLDKLRAEIAINVHLDLTKV 473
Qy	523	DLFGCDTQMIYDMLRLKSVLYLPDGFVCKGEIKGEMWIIKHGEVQVLGGPDGPKVLV 582
Db	474	RIFADCEAGLLVELVLKLPQVSPGDIYCKKGDIGREMYIIKEGLAVV-ADDGVTQFV 532
Qy	583	TLKAGSVFGESILLAAGG---GNRRTANVVAHFANLLTLDKTLQELVHYHYPDSERILM 639
Db	533	VLSGSGVFGISILINIKSGKAGNRRRTANIRSIGSDLFCLSKDDLMEALTEYDPDKTMLE 592
Qy	640	KKARVLLKQKA---KTAETATPPRKDLALLFPKKEETPKLFTKLGGTGKASLARLL--- 692
Db	593	EKGQILMKDGLDLNANAGSDPKOLEEKVTRMEGSDVLQT-----RPARILAEY 644
Qy	693	-----KLKRFQAQK-----ENSEG-GREG 713
Db	645	ESMQQKLQRLTKVEKFLKPLIDTFESIEGPGAESG 681
RESULT 10		
JH0560		
cyclic nucleotide-gated channel - channel catfish		
C;Species: Ictalurus punctatus (channel catfish)		
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004		
C;Accession: JH0560		
R;Goulding, E.H.; Ngai, J.; Kramer, R.H.; Colicos, S.; Axel, R.; Siegelbaum, S.A.; Ches		
Neuron 8, 45-58, 1992		
A;Title: Molecular cloning and single-channel properties of the cyclic nucleotide-gated		
A;Reference number: JH0560; MUID:92110008; PMID:1370374		
A;Accession: JH0560		
A;Molecule type: mRNA		
A;Status: nucleic acid sequence not shown		
A;Residues: 1-682 <GOU>		
A;Cross-references: UNIPROT:P55934; GB:M03111		
A;Experimental source: olfactory epithelium		

Query Match		19.1%; Score 807.5; DB 1; Length 682;
Best Local Similarity		29.0%; Pred. No. 5.3e-42;
Matches		192; Conservative 137; Mismatches 256; Indels 77; Gaps 17;
Qy	119	PAAPVINEYAD---AQLHNLVKRMQRORTALYKKLVEGDLSSPEA-----SPQTAKPT 168
Db	55	PSAEMLEAFTQRRPLARLVNLVLSREWA---HKSIVETE-QRPDSFLERFRFGPQAANDQ 110
Qy	169	AVPPVKESDDKPTHEHYRYLLWFKVKKMPLETEYLKRIKLPNSIDSYDRLYLWLLLVTLA 228
Db	111	SAAPA---DAPKTF-----KRWEGFVVQSDDIYYWLFIALA 148
Qy	229	--YNNCWFIPRLVFPYQTADNIHLYADIICDIILYDMLFIQPRLOFVRGGDIIVD 286
Db	149	SLYNW--IMVARACFDQLQDENFFLWGLDVLCDVIYILDTC-IRLRTGYLEQGLLVKD 205
Qy	287	SNELRKHYSITKFDVASIIPFDICVLPFGFNPMFRANRMLKYTSFEFNHHLESIMD 346
Db	206	LAKLRDNYIRTLQFKLDLFLSIPTTELLFFVTGVQPLRFNRLLRFRMPEFFDRTETRN 265
Qy	347	KAVYRVIRTTGYLLFILHINACVYVWASNYEGIGTRTWYDGEKNE---YLRCYVWAV 402
Db	266	YNAPFRICNLILYLVIIHWNACIYVAISKALGLSDTWYSGQNTLSFCYVYCYFWST 325
Qy	403	RTLITIGLPEPQTLPEIYFOLLNFPFSGVVFSSLIGOMRDVIGATANQNYFRACMDDT 462
Db	326	LTLTTIGEMPPPVKDBEYVVFVDFLVGLVIFATIVGNVGSMIANNMNAARAEFQTRIDAI 385
Qy	463	IAYMNNYSIPKLQKRVRTWYETWDSORMDESLLKTLPTTVQLALAIQVNFISIISKV 522
Db	386	KYMHPRKNVTRLETREVIKWFYLDWTKVTDEQEVKLNLPDKLRAEIAINVHLDLTKV 445
Qy	523	DLFGCDTQMIYDMLRLKSVLYLPDGFVCKGEIKGEMWIIKHGEVQVLGGPDGPKVLV 582
Db	446	RIFQDCEAGLLVELVLKLPQVSPGDIYCRKGDIGKEMWIIKEGLAVV-ADDGVTQFA 504
Qy	583	TLKAGSVFGESILLAAGG---GNRRTANVVAHFANLLTLDKTLQELVHYHYPDSERILM 639
Db	505	LLTAGSCFGEISILNITQSGKMGNRRRTANIRSIGSDLFCLSKDDLMEAVAEVPAQKVL 564
Qy	640	KKARVLLKQKATAEATP-----PRKDLALLFPKKEETPKLFTKLGG---GT 683
Db	565	ERGRETILRKQGLDDESVAAAGLGVIDTEKVERLDASL-----DILQTRFARLLGEFTST 619
Qy	684	GKASLARLLKREQA---AQKENSEGEEEG---KENEDKQKENEKQENEDKGE 736
Db	620	QRLRKQRTALERQLCHTGLGLLSONEAGEHAGVPTHTHADIIHAQPETHTRTSAETNSE 679
Qy	737	NE 738
Db	680	EE 681
RESULT 11		
SL1517		
cyclic nucleotide-activated channel protein - rat		
C;Species: Rattus norvegicus (Norway rat)		
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004		
C;Accession: SL1517		
R;Dhallan, R.S.; Yau, K.W.; Schrader, K.A.; Reed, R.R.		
Nature 347, 184-187, 1990		

A>Title: Primary structure and functional expression of a cyclic nucleotide-activated ch  
A/Reference number: S11517; MUID:90370115; PMID:1697649  
A/Accession: S11517  
A/Molecule type: mRNA  
A/Residues: 1-664 <DNA>  
A/Cross-references: UNIPROT:Q00195; GB:X55519; NID:956791; PIDN:CAA39135.1; PID:956792  
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-  
C:Keywords: transmembrane protein  
F:456-580/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>  
Query Match 19.0%; Score 804; DB 2; Length 664;  
Best Local Similarity 29.6%; Pred. No. 8.5e-42;  
Matches 219; Conservative 126; Mismatches 286; Indels 108; Gaps 22;  
QY 50 ESKLTKTPVTSEPHNTIADKSKSSGGLTTPDPQNAAEPTGTVEQK---EMDP 106  
DB 4 EKSNGVKSPANN---HNHPPPSIKANGKDDHRAGRPSQVAADDTSPELQRLAEMDT 60  
QY 107 GKEGPNSPQKPPAAPVINEYADAQH-----NLVGRMORTALYKKKLVEGLSSPE 159  
DB 61 PRGRGGFQRIVRLVGVIRDMANKNFRREEPRDPSFLERF-----GPE 104  
QY 160 ASPTAKPTAVPVKESDDKPTHEHYRLLWFKVKMPLTEYLKRIKLPNSIDSYTDRLYL 219  
DB 105 LQTVTHOGDDKGGDGGKGTGKKFELF-----VLDPAGD-WY 143  
QY 220 LWLLAVTL--AYNNWCNFIPLRLVFPYQTDADNIHWLIADIICDIILYDMLFIQRLQF 277  
DB 144 RWFVIAMPVLYNW-CLLV-ARACSDIQRNVFVWLVLDYFSDIVYIAD-LIIRLTGF 200  
QY 278 VGGDIIIVDSNELRKHRTSTKFQDVAIIIPDCIYLPFGF-NPMFRANRLKYSFPE 336  
DB 201 LEQGLLVKDPKRLRNYHTLQFKLDVAIIPTDLIYPAVGHISPEVFRNLLHPARFE 260  
QY 337 FNHHLESIMDKAYIRVIRTTCYLLFILHINACVYVWASNYEGITRWY----DGE-- 390  
DB 261 FDRTEHTSTPNIFRISNLVLIIVIHWNACIYVVISKSIQFGVDTPVYVNIIDPYG 320  
QY 391 --GNEYLCRYWAVRTLTITIGLPEPQTLFEIVFOLLNFFSGVFVSSLIQGMRDVIGAA 448  
DB 321 VLAREYIYCLYWSLTLTITIGETPPVVDKDEVLVFIQDLGLVIFATIVGNVSGMISNM 380  
QY 449 TANQNYFRACDDTTIAYNNYSIPKLQKRVRTWYETWDSQORMDESDLLKTLPTTVOL 508  
DB 381 NATRAEFOAKIDAVHYMQFRKVSXDMKAVIKWPDYLTWTKTVDEREVLKNPAPLRA 440  
QY 509 ALAIDVNFSLISKVDLFKGCOTQMIYDMLRLKSLVLYLPGDPVCKKGIGKEMYYIKGE 568  
DB 441 EIAINVLHSTLKKVRIFODCEAGLLVELVLKLPQVFGSDYICRKGDIGKEMYYIKEGK 500  
QY 569 VQVLGGPDGTKVLVTLKAGSVFGEISLLAAG--GNRRANVVAHGFANLLTLDDKTLQ 625  
DB 501 LAVV-ADGVVTQYALLSAGSCFGEISILNIGSKWGNRTANIRSLGYSDFCLSKDLM 559  
QY 626 EILVHYPSERILMKARVLLKQAKTAE---ATPPKDLALLPPKPEETPKLFKTLGG 682  
DB 560 BAVTEYDPAKVLBERGEILMKEGLLDENEAASMEVDV-----QSKLEQLETNM--D 611  
QY 683 TGKASLALLKLRQAQAKKENSEGGEKENEKEDKQEN--EDKQKENEKEDKQENEDK 740  
DB 612 TLYTRFARLL-----ABYTAQOQKLKQRIITVLETKMKNH-----EDDYL 651  
QY 741 DKGREPEKPLDRPCECTAS 759  
DB 652 SDG-----INTPEPTAA 663

RESULT 12

JC6509

rod cyclic nucleotide-gated cation channel protein alpha-chain - dog

C/Species: Canis lupus familiaris (dog)

C/Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 09-Jul-2004

C/Accession: JC6509

R.Veske, A.; Nilsson, S.E.G.; Gal, A.

Gene 202, 115-119, 1997

A/Title: Characterization of canine rod photoreceptor cGMP-gated cation channel alpha-sub

A/Reference number: JC6509; MUID:98087425; PMID:9427553

A/Accession: JC6509

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-691 <VES>

A/Cross-references: UNIPROT:Q28279; EMBL:X99914; NID:91488571; PIDN:CAA68186.1; PID:9148

C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

F:478-602/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 18.9%; Score 801.5; DB 2; Length 691;  
Best Local Similarity 29.2%; Pred. No. 1.3e-41;  
Matches 220; Conservative 136; Mismatches 286; Indels 112; Gaps 23;  
QY 21 EQSRRNEEGSHPSNQSOQTAAQENKGEESLTKTPTVTSEPHNTIADKSKNSG 80  
DB 24 EKEIRRMENGARSS-----FSDDDDDDSDASMFEE---ENETPHA--RDSCRNSQRR 72  
QY 81 DLTTNPDPQNAAEPTGTVEQKEMDPGKEGPNSPQKPPAAPVINEYADAQLHNLVKRMR 140  
DB 73 D-----PSQRE-----QYLPGAIALFNWNSSNKEQEPKKEK 104  
QY 141 QRTALYKKLVEGLSSPEASPTAKPTAVPVKESDDKPTHEHYRLLWFKVKMPLTEY 200  
DB 105 KKKK--EKKSXSGDKNENKDSKKKKE---KEKEKKNKEK-----GKDKK---EEE 150  
QY 201 LKRIKLPNSIDSYTDRLYLLWLLVTL--AYNNWCNFIPLRLVFPYQTDADNIHWLIADI 258  
DB 151 KKEVMV---IDP-AGNMYNNLFCITLFPVMYNT--MVIARACFDQLQSDYLEWIIIFY 204  
QY 259 ICDIILYDMLFIQRLQFVRGGDIIIVDSNELRKHRTSTKFQDVAIIIPDCIYLPFG 318  
DB 205 LSDIVYLLDM-FVTRTGYLEQGLLVREAEKLEIKYKSNLQFKLDLSVITDILLYFKLG 263  
QY 319 FN-PMFRANRLKYSFPEFNHLESIMDKAYIRVIRTTCYLLFILHINACVYVWASNY 377  
DB 264 WNYFEIRNLRLRISRMFEFPQRTETRTNYPNIFRISNLVMIYVIIHWNACVYFISKA 323  
QY 378 EGIGTTRWY----DGE-----GNEYLCRYWAVRTLTITIGLPEPQTLFEIVFOLLNFFS 429  
DB 324 IGFNGDTPVYVNDPEFGLRLARKYVSLYWSLTLTITIGETPPVVDSEYFVVDVFLI 383  
QY 430 GVVFSSLIQGMRDVIGAAATANQNYFRACDDTTIAYNNYSIPKLQKRVRTWYETWDS 489  
DB 384 GVLFIATIVGNISNMNNAARAEFQARIDAIQYWHFRNVSKDMKRVIKWFDYLTWN 443  
QY 490 QRMLEDSDLLKTLPTTVQLALADVNFSLISKVDLFKGCOTQMIYDMLRLKSLVLYLPGD 549  
DB 444 KKTVDKEVLKLPDLKRAETAINVHLDTLKKVRIFADCEAGLLVELVLKLPQVYSPGD 503  
QY 550 FVCKKGIGKEMYYIKGEVOVLGGPDGTKVLVTLKAGSVFGEISLLAAG--GNRRTA 606  
DB 504 YICKKGIGKEMYYIKGEKLAUV-ADGIGITQFVVLSDGSYFGEISILNIGSKAGNRRTA 562  
QY 607 NVVAHGFANLLTLDDKTLQETLVHYPSERILMKARVLLKQAKTAE---KTAEATPPKDL 662  
DB 563 NIKSIGYSDFCLSKDLMLEALTEYDPAKTLMBEGKQILMKOGLLDINIANAGSDPKDL 622  
QY 663 ALLFPKPEETPKLFKTLGGTGKASLARLLKLRQAQAKKENSEGGEKENEKEDKQKE 722  
DB 623 EEKVTMRMEGSDVLLAQT-----RPARIL-----AEYESMQOK 653  
QY 723 NEDQKQENEDKQENEDK-----KGREPEEKPLD 752  
DB 654 LKQRLTKVERFLKPIIDTFPSALEGTGDSRPLD 687

RESULT 13

S07103

cGMP-gated ion channel protein - bovine

C/Species: Bos primigenius taurus (cattle)



```

Db      548  VV-AEDGTFQVVLGDGSGVFGISILNINIKGSKGNRRNTANIRSGYDLFCLSKDDLMEA 606
Qy      628  LVHYDPSERIIMKKAR-VLLKQK---AKTATPPKDLALIFPPKEETPKLFKTLGGT 683
Db      607  LTEYPEAKKALEKGRQILMKDNLDEELAKAGAPKDI-----EEKVEHLETSLSL 659
Qy      684  GKASLARLL-----KLKREQAAQKEN 705
Db      660  -QTRFARLLAEYNATQMKVQKRLSLES 686

RESULT 15
150680
alpha subunit of rod photoreceptor CNG-channel - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50680
R:Bonigk, W.; Altenhofen, W.; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; Kaupp, U.B
Neuron 10, 865-877, 1993
A:Title: Rod and cone photoreceptor cells express distinct genes for cGMP-gated channels
A:Reference number: I50630; MUID:93264082; PMID:7684234
A:Accession: I50680
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-645 <BON>
A:Cross-references: UNIPROT:Q90980; EMBL:X89599; NID:G908852; PIDN:CAA61758.1; PID:G9088
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
F:431-555/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match      18.2%; Score 771; DB 2; Length 645;
Best Local Similarity 34.3%; Pred. No. 8.7e-40;
Matches 173; Conservative 104; Mismatches 196; Indels 32; Gaps 12;

Qy      217  LYLWLLLVLT--AYNWCWFIPLRVPYQYQADNIHWLIADIICDIIYLYDMLFIQPR 274
Db      116  MYNWLFCITWPMVNWNT--MIARACFDEQNDYLAWFIVDVSDVIYIADM-FVETR 172
Qy      275  LQFVRGGDIIVDSNELRKHRTSTKFDLDAVSIIPFDICYLFFGFN-PMFRANRLKYTS 333
Db      173  TGYLEQGLLVKEEQKLEKYKSSQLQKLDLFIPTDLLYFKLGLNYPELRINLLRVAR 232
Qy      334  FFEFNHLESIMDKAYIVRVITRTGYLLFILHNACVYWNASNYEGIGTTRWVYDGEQN- 392
Db      233  MFEFFQRTETRTNVPNIFRISNLVMIYIIHWNACVYYSISKAIGFGADTWVPNTSHP 292
Qy      393  -----EYLRCYYWAVTLITIGLPEPQTLFEIVFOLLNFFSGVFVFSLLIGMRDVI 445
Db      293  EFARLTRKYVSYLWSTLTITIGTPPPVRDSEYFFVVVDVFLVGLVIFATIVGVGSMI 352
Qy      446  GAATANQNYFRACMDDTIAYNNYSIPKLQKRVRTWYETWDSQRMDELDESLLKLTPTT 505
Db      353  SNMNAARAEFOAKIDAIKQYMHFRNVSKMEKVKWFDYLTWNKKAVDREVLYKLPDK 412
Qy      506  VOLALADVNFISIISKVDFKCDTQMIYDMLLRKSVLYLPGDPVCKKGIGKEMYIIK 565
Db      413  LRAETAINVHLETLKKRIFADCEAGLLVELVLQPOVSPGYICRKGDIGREMYIIK 472
Qy      566  HGEVQVLGGPDGTVLTKAGSVGEISLLAAG--GNERTANVAHGFANLLTLDDK 622
Db      473  EGKLAW--ADGVTQFVVLSDGSGVFGISILNINIKGSKGNRRNTANIRSIGYDLFCLSKD 531
Qy      623  TLQETLVHYPDSERIIMKKAR-VLLKQKAKTAEATPPRKDLALLFPKKEETPKLFKTLG 681
Db      532  DLMEALTEYPAKAMLEKKGQILMKDGLLDIEVANLGSD-----PKOLEKV--AYME 583
Qy      682  GTG---KASLARLLKLKREQAAQKK 703
Db      584  GMDRLQTKFARL--LAEYDAQAQK 606
```

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 27, 2005, 18:08:36 ; Search time 130 Seconds  
(without alignments)  
3186.708 Million cell updates/sec

Title: US-09-855-828-1

Perfect score: 4234

Sequence: 1 MFKSLTKVKNKVPIGENNEN.....PSAEGGEVLTVKKEKAKQ 809

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4234	100.0	809	1	CNB3 HUMAN
2	3181.5	75.1	782	1	CNB3 CANFA
3	2515	59.4	694	1	CNB3 MOUSE
4	1971.5	46.6	866	2	Q80XL8 mus musculus
5	1959	46.3	1339	2	O35788 rattus norv
6	1952	46.1	1245	2	O43636 homo sapien
7	1949	46.0	909	1	CNG4 HUMAN
8	1949	46.0	1251	2	Q9UMG2 homo sapien
9	1923	45.4	858	2	O55157 rattus norv
10	1920	45.3	938	2	O77658 bos taurus
11	1920	45.3	948	2	O77659 bos taurus
12	1920	45.3	952	2	O77660 bos taurus
13	1920	45.3	1394	1	CNG4 BOVIN
14	1103	26.1	1040	2	Q9W2D5 drosophila
15	1096	25.9	800	2	P90975 caenorhabdi
16	1095	25.9	800	2	P90975 mus taurus
17	878	20.7	515	2	Q95SL0 drosophila
18	850	20.1	694	1	CNG3 HUMAN
19	831.5	19.6	683	1	CNG1 RAT
20	829	19.6	663	1	CNG2 BOVIN
21	826.5	19.5	698	2	Q6ZNA7 homo sapien
22	823.5	19.4	684	1	CNG1 MOUSE
23	821.5	19.4	735	1	CNG1 CHICK
24	818.5	19.3	664	1	CNG2 RABIT
25	818	19.3	686	2	CNG1 HUMAN
26	817	19.3	686	1	CNG1 HUMAN
27	807.5	19.1	682	1	CNG ICTPU
28	806	19.0	611	2	Q9QWV7 rattus norv
29	806	19.0	632	2	Q9ER32 rattus norv
30	806	19.0	670	2	Q9ER33 rattus norv
31	804	19.0	664	1	CNG2 RAT

32	801.5	18.9	691	1	CNG1 CANFA
33	797	18.8	690	1	CNG1 BOVIN
34	794	18.8	706	1	CNG3 BOVIN
35	789.5	18.6	664	2	Q80XH6 mus musculus
36	788.5	18.6	631	1	CNG3 MOUSE
37	788.5	18.6	631	2	Q8CFV6 mus musculus
38	788.5	18.6	733	1	CNG CABEL
39	787.5	18.6	1218	2	Q9W201 drosophila
40	783.5	18.5	637	2	Q80416 carassius a
41	777.5	18.4	664	1	CNG2 MOUSE
42	771	18.2	645	1	CNG3 CHICK
43	768.5	18.2	799	2	Q7PTE6 gallus gall
44	759	17.9	1453	2	Q8IR35 anopheles g
45	759	17.9	1463	2	Q9U5E2 drosophila

#### ALIGNMENTS

RESULT 1  
CNB3 HUMAN  
ID CNB3 HUMAN STANDARD; PRT; 809 AA.  
AC Q9NCW8; Q9NRE9;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Cyclic-nucleotide-gated cation channel beta 3 (CNG channel beta 3)  
DE (Cyclic nucleotide-gated channel beta 3) (Cone photoreceptor cGMP-gated channel beta subunit) (Cyclic nucleotide-gated cation channel modulatory subunit).  
DE Name=CNGB3;  
GN Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, VARIANT ACHM3 PHE-435, AND VARIANTS PRO-298 AND GLY-755.  
RX MEDLINE=20414632; PubMed=10958649; DOI=10.1093/hmg/9.14.2107;  
RA Kohl S., Baumann B., Broghammer M., Jaegle H., Sieving P., Kellner U., Spegal R., Anastasi M., Zrenner E., Sharpe L.T., Missinger B.;  
RT "Mutations in the CNB3 gene encoding the beta-subunit of the cone photoreceptor cGMP-gated channel are responsible for achromatopsia (ACHM3) linked to chromosome 8Q21.";  
Hum. Mol. Genet. 9:2107-2116(2000).  
[2]  
RP SEQUENCE OF 114-809 FROM N.A. (ISOFORM 2), FUNCTION, SUBUNIT, VARIANT ACHM3 PHE-435, AND VARIANT CYS-234.  
RC TISSUE=Retina;  
RX MEDLINE=20347712; PubMed=10888875; DOI=10.1038/77162;  
RA Sundin O.H., Yang J.-M., Li Y., Zhu D., Hurd J.N., Mitchell T.N., Silva E.D., Maunee I.H.;  
RT "Genetic basis of total colourblindness among the Pingelapese islanders.";  
Nat. Genet. 25:289-293(2000).  
-1- FUNCTION: Visual signal transduction is mediated by a G-protein coupled cascade using cGMP as second messenger. This protein can be activated by cGMP which leads to an opening of the cation channel and thereby causing a depolarization of rod photoreceptors. Induced a flickering channel gating, weakened the outward rectification in the presence of extracellular calcium, increased sensitivity for L-cis diltiazem and enhanced the cAMP efficiency of the channel when coexpressed with CNGA3 (by similarity). Essential for the generation of light-evoked electrical responses in the red-, green- and blue sensitive cones.  
-1- SUBUNIT: Heterooligomeric complex with CNGA3.  
-1- SUBCELLULAR LOCATION: Integral membrane protein.  
-1- ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=2;  
Name=1;  
IsoId=Q9NCW8-1; Sequence=Displayed;  
Name=2;  
IsoId=Q9NCW8-2; Sequence=VSP\_009742;

CC Note=No experimental confirmation available;  
 CC -I- TISSUE SPECIFICITY: Expressed specifically in the retina.  
 CC -I- DISEASE: Defects in CNGB3 are a cause of achromatopsia 3 (ACHM3)  
 CC [MIM:262300]; also known as Pingelapese blindness. ACHM3 is a  
 CC congenital complete achromatopsia and is distinct from total  
 CC colorblindness mainly because of the consistent concurrence of  
 CC severe myopia.  
 CC -I- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel  
 CC (TC 1.A.1.5) family.  
 CC -I- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AF272500; AAF86274.1; -;  
 CC EMBL: AF228520; AAF80179.1; ALT\_INIT.  
 CC Genew; HGNC:2153; CNGB3.  
 CC MIM: 262300; -;  
 CC InterPro: IPR00595; cNMP binding.  
 CC InterPro: IPR005821; Ion Trans.  
 CC InterPro: IPR001622; K+channel\_pore.  
 CC Pfam: PF00027; cNMP\_binding; 1.  
 CC SMART: SM00520; Ion\_trans; 1.  
 CC SMART: SM00100; cNMP; 1.  
 CC PROSITE: PS00889; CNMP\_BINDING\_1;  
 CC PROSITE: PS00888; CNMP\_BINDING\_2; 1.  
 CC PROSITE: PS50042; CNMP\_BINDING\_3; 1.  
 CC KW Alternative splicing; cGMP-binding; Disease mutation; Ion transport;  
 CC Ionic channel; Multigene family; Polymorphism; Transmembrane; Vision.  
 FT DOMAIN 1 216  
 FT TRANSMEM 217 237  
 FT DOMAIN 238 250  
 FT TRANSMEM 251 271  
 FT DOMAIN 272 302  
 FT TRANSMEM 303 323  
 FT DOMAIN 324 359  
 FT TRANSMEM 360 380  
 FT DOMAIN 381 417  
 FT TRANSMEM 418 438  
 FT DOMAIN 439 504  
 FT TRANSMEM 505 525  
 FT DOMAIN 526 609  
 FT NP\_BIND 532 676  
 FT BINDING 592 592  
 FT BINDING 604 604  
 FT CARBOHYD 468 468  
 FT VARSPPLIC 590 594  
 FT VARIANT 234 234  
 FT VARIANT 298 298  
 FT VARIANT 435 435  
 FT VARIANT 755 755  
 FT SEQUENCE 809 AA; 92249 MW; AC23B7072C1C7DB3 CRC64;  
 Query Match 100.0%; Score 4234; DB 1; Length 809;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-229;  
 Matches 809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MFKSLTKVNVKVPDGENNEQSRNEGSHPSNQSQOQTAEENKGREKSLTKKSTPV 60  
 DB 1 MFKSLTKVNVKVPDGENNEQSRNEGSHPSNQSQOQTAEENKGREKSLTKKSTPV 60  
 QY 61 TSEBPHNTIQDKLSKKNSSGDLTTNPDQNAEPTGTVPQKEMDPGKEGPNSPQNKPPA 120

DB 61 TSEBPHNTIQDKLSKKNSSGDLTTNPDQNAEPTGTVPQKEMDPGKEGPNSPQNKPPA 120  
 QY 121 AVINEYADAQLHNLVKRMORQTALYKKLVGDLSSPEASPTAKPTAVPPVKESDDKP 180  
 DB 121 AVINEYADAQLHNLVKRMORQTALYKKLVGDLSSPEASPTAKPTAVPPVKESDDKP 180  
 QY 181 TBHYRLRLWFKVKWMPLEYLKRILKPNISDSYTDRLYLWLLVTLAYNNWCWFIPLRL 240  
 DB 181 TBHYRLRLWFKVKWMPLEYLKRILKPNISDSYTDRLYLWLLVTLAYNNWCWFIPLRL 240  
 QY 241 VFPYQADNIHWLIADIICDIYYIDMLFIQPRQFVRGGDIIVDSNELKHYRTSTKF 300  
 DB 241 VFPYQADNIHWLIADIICDIYYIDMLFIQPRQFVRGGDIIVDSNELKHYRTSTKF 300  
 QY 301 QLDVASIIPFDICYLFFGNPMFRANMLKYTSFEFNHLESIMDKAYIVIRITGYL 360  
 DB 301 QLDVASIIPFDICYLFFGNPMFRANMLKYTSFEFNHLESIMDKAYIVIRITGYL 360  
 QY 361 LFIILINACVYVWASNYEGITGRVWYDGEQNEYLRCYYWAVRTLITIGGLPEPQTLFEI 420  
 DB 361 LFIILINACVYVWASNYEGITGRVWYDGEQNEYLRCYYWAVRTLITIGGLPEPQTLFEI 420  
 QY 421 VFQLLNFFSGVVFVSSLIQOMRDVIGATATANQNYFRACMDDTIAYNNYSIPKLQKRV 480  
 DB 421 VFQLLNFFSGVVFVSSLIQOMRDVIGATATANQNYFRACMDDTIAYNNYSIPKLQKRV 480  
 QY 481 TWYEYTWDSQRMDESLLKTLPTVOLALADVNFISIISKVDLPKGCOTMIYDMLLRL 540  
 DB 481 TWYEYTWDSQRMDESLLKTLPTVOLALADVNFISIISKVDLPKGCOTMIYDMLLRL 540  
 QY 541 KSVLYLPDGFVCKKGEGIKEMWIIKHGEVQVLGGPDGTVLTKAGSVFGEISLLAAG 600  
 DB 541 KSVLYLPDGFVCKKGEGIKEMWIIKHGEVQVLGGPDGTVLTKAGSVFGEISLLAAG 600  
 QY 601 GNRRTANVVAHGFANLLTLDKKTQILVHYVDPDSERILMKARVLLKQAKTAEATPPRK 660  
 DB 601 GNRRTANVVAHGFANLLTLDKKTQILVHYVDPDSERILMKARVLLKQAKTAEATPPRK 660  
 QY 661 DLALLFPPEETPKLFTLLGGTGKASLARLLKLKREQAQKENSEGEEGKENEKQ 720  
 DB 661 DLALLFPPEETPKLFTLLGGTGKASLARLLKLKREQAQKENSEGEEGKENEKQ 720  
 QY 721 KENEDKQKENEKQKENEKQKREPEEKPLDRPECTASPIAVEEPHSVRRITVLPRTS 780  
 DB 721 KENEDKQKENEKQKENEKQKREPEEKPLDRPECTASPIAVEEPHSVRRITVLPRTS 780  
 QY 781 RQSLIISMAPSAGGEEVLTIIVKSKAKQ 809  
 DB 781 RQSLIISMAPSAGGEEVLTIIVKSKAKQ 809  
 RESULT 2  
 CNB3\_CANFA STANDARD; PRT; 782 AA.  
 ID CNB3\_CANFA  
 AC Q8MJU7;  
 DT 29-MAR-2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Cyclic-nucleotide-gated cation channel beta 3 (CNG channel beta 3)  
 DE Cyclic nucleotide-gated channel beta 3 (Cone photoreceptor cGMP-  
 DE gated channel beta subunit) (Cyclic nucleotide-gated cation channel  
 DE modulatory subunit).  
 GN Name=CNGB3;  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND VARIANT CD ASN-262.  
 RX PubMed=12140185; DOI=10.1093/hmg/11.16.1823;  
 RA SidJanin D.J., Lowe J.K., McElwee J.L., Milne B.S., Phippen T.M.,  
 RA Sargan D.R., Aguirre G.D., Acland G.M., Ostrander E.A.;

QY 60 VISBEPHINTQAKSIAKSSSGULTINPDPQNAAEFIGIVFEQKREMDPFGKGFNFQNNKFQY

KA  
KA  
RT  
gerischer A., Zong X., Holmann F., Bier M.,  
"Molecular cloning and functional characterization of a new modulatory

RT cyclic nucleotide-gated channel subunit from mouse retina.";

RL J. Neurosci. 20:1324-1332(2000).

CC -|- FUNCTION: Visual signal transduction is mediated by a G-protein

CC coupled cascade using cGMP as second messenger. This protein can

CC be activated by cGMP which leads to an opening of the cation

CC channel and thereby causing a depolarization of rod

CC photoreceptors. Essential for the generation of light-evoked

CC electrical responses in the red-, green- and blue sensitive cones

CC (by similarity). Induced a flickering channel gating, weakened the

CC outward rectification in the presence of extracellular calcium,

CC increased sensitivity for L-cis diliazem and enhanced the cAMP

CC efficacy of the channel when coexpressed with CNGB3.

CC -|- SUBUNIT: Heterooligomeric complex with CNGB3.

CC -|- SUBCELLULAR LOCATION: Integral membrane protein.

CC -|- TISSUE SPECIFICITY: Small subset of retinal photoreceptor cells and

CC testis.

CC -|- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel

CC (TC 1.A.1.5) family.

CC -|- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

CC -----

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CC -----

DR EMBL; AJ243572; CAB71152.1; -.

DR MGD; MGI:1353562; CnGB3.

DR GO; GO:0005886; C:Plasma membrane; IC.

DR GO; GO:0030553; F:3', 5'-cGMP binding; IC.

DR GO; GO:0005223; F:intracellular cGMP activated cation channel. . .; IPI.

DR GO; GO:0009187; P:Cyclic nucleotide metabolism; IC.

DR InterPro; IPR000595; cNMP binding.

DR InterPro; IPR005821; Ion trans.

DR InterPro; IPR001622; K+channel\_pore.

DR Pfam; PF00027; cNMP binding; 1.

DR Pfam; PF00520; Ion trans; 1.

DR SMART; SM00100; cNMP; 1.

DR PROSITE; PS00888; CNMP BINDING\_1; 1.

DR PROSITE; PS00889; CNMP BINDING\_2; 1.

DR PROSITE; PS50042; CNMP BINDING\_3; 1.

DR cGMP-binding; Ion transport; Ionic channel; Multigene family;

KW Transmembrane; Vision

FT DOMAIN 1 209 Cytoplasmic (Potential).

FT TRANSMEM 210 230 H1 (Potential).

FT DOMAIN 231 242 Extracellular (Potential).

FT TRANSMEM 243 263 H2 (Potential).

FT DOMAIN 264 294 Cytoplasmic (Potential).

FT TRANSMEM 295 315 H3 (Potential).

FT DOMAIN 316 351 Extracellular (Potential).

FT TRANSMEM 352 372 H4 (Potential).

FT DOMAIN 373 409 Cytoplasmic (Potential).

FT TRANSMEM 410 430 H5 (Potential).

FT DOMAIN 431 568 Extracellular (Potential).

FT TRANSMEM 569 589 H6 (Potential).

FT DOMAIN 590 694 cNMP (By similarity).

FT NP\_BIND 524 668 cGMP (By similarity).

FT BINDING 584 584 cGMP (By similarity).

FT BINDING 596 596 cNMP (By similarity).

FT CARBOHYD 507 507 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 694 AA; 79722 MW; 0B9F9CF3B180DA82 CRC64;

Query Match 59.4%; Score 2515; DB 1; Length 694;

Best Local Similarity 68.7%; Pred. No. 4.4e-133;

Matches 485; Conservative 92; Mismatches 113; Indels 16; Gaps 7;

Qy 1 MFKSLT-KVNVKPIGNNENEGSRGHP--SNOSQQTAAQENKGEKSLTKTS 57

Db 1 MLKSLTKVFNKVPNM-----EGRMKKLCNLSLSQPTAAGDQSQEPLRSR- 50

Qy 58 TPVTSEPHNTIQDLKSKKNSGDLTTNPDQNAABPTGTVPRQKMDFGKGNPQNK 117

Db 51 TPITPEKSHK-EDNSTGNSLRDFTPNPDPECRABLTTRTMAEMEKTRTKRPPVSFKTK 109

Qy 118 PPAAPVINEYADAOLHNLVKRMORTALYKKLVEGD-LSSPEASQTAKPATVPPVKES 176

Db 110 VLETSIINEYTAHNLHNLVRRMERTALYKKTLTBEENFEVEASQTAAMSTNISPKQEN 169

Qy 177 DKPTEHYVRLWFKVKMPLTEYLKRIKLPSIDSIDYDRLVLLMLLLVLTAYNNCWFI 236

Db 170 NSKLKEH-QDTSFQKQPVVKEHLRMLPLPSIDSIDYDRLVLLMLLLVLTAYNNCWLL 228

Qy 237 PLRLVFPYQADNIHYWLIADICDIYLYDMLFIQPRLOQFVRGGDIIVDSNELRKHRT 296

Db 229 PVRLVFPQCPDNKNYWIITDVCIDIILLIQPRLOQFVRGGDIIVDSNELKRNYS 288

Qy 297 STKFQLDVASIIPFDICYLFGFNPMFRANRMLKYSFPEFNHLESIMDKAYIRVIRT 356

Db 289 STKFRMDVASLPEFLVYIFFGNPIFRANRILKYSFPEFNHLESIMDKAYVVRVIRT 348

Qy 357 TGYLLFILHINACVYVWASNYEGIGTRVWYDGEYVYVWVAVRTLTITIGGLPEPOT 416

Db 349 TGYLLFILHINACVYVWASDYEGISTKWNVNGEYVYVWVAVRTLTITIGGLPEPOT 408

Qy 417 LFEIVFQLNFFSGVVFSSLLIGQMRDVIQATATQNYFRACMDPTIAYMNNYSIPKLVO 476

Db 409 SFEIVFQPLNFFSGVVFSSLLIGQMRDVIQATATQNYFRACMDHIIAYMKNYSIPQSVQ 468

Qy 477 KVRVWYETWDSQRMDESLLKTLPTVLOALADVNFSIISKVDLFGKCDTQMIYDM 536

Db 469 YRVWLTWYTNWSQRLDESLLNLTPTAMQSLADINFSIIDKVELFGKCDTQMIYDL 528

Qy 537 LLRLKSLVLPDGFVCKKGEIGKEMVYIKHGVQVLGGDGTQVLVTLKAGSVFGEISLL 596

Db 529 LLRLKSTVLPDGFVCKKGEIGKEMVYIKHGEVQVLGGDGAQVLVTLKAGSVFGEISLL 588

Qy 597 AAGGGRRTANVVAHGFANLLTDKKTQLLEIIVHYVPSERILMKKARVLLKQAKTAET 656

Db 589 AXGGGNRRRTADVVAHGFANLLTDKKTQLLEIIVHYVPSERILMKKARVLLKQAKTQAI 648

Qy 657 PPRKDLALLFPPEKEETPKLFTLLGGTGKASLARILLKLRQAAQK 702

Db 649 PARPGPAFLFPPEKEETPRMLKVLGNTGKVDLGRLLKGRKRTTQK 694

RESULT 4

Q80XL8 PRELIMINARY; PRT; 866 AA.

ID Q80XL8

AC Q80XL8

DT 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE CnGB1b protein (Fragment).

GN Name=CnGB1b;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

OX [1]

RN SEQUENCE FROM N.A.

RP

RC TISSUE=Eye;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,

RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny N.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RC Director: MGC Project;
RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC045114; AAH45114.1; -
DR HSSP; O88703; 1043.
DR MGD; MGI:2664102; Cngb1b.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005216; P: ion channel activity; IEA.
DR GO; GO:0006811; P: ion transport; IEA.
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00027; cNMP binding; 1.
DR Pfam; PF00520; Ion_trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; UNKNOWN_1.
DR PROSITE; PS00889; cNMP_BINDING_2; 1.
DR PROSITE; PS50042; cNMP_BINDING_3; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT NON_TER 1
SQ SEQUENCE 866 AA; 97427 MW; CACCA4AD8EB6DEE2A CRC64;

Query Match 46.6%; Score 1971.5; DB 2; Length 866;
Best Local Similarity 47.5%; Pred. No. 2e-102;
Matches 406; Conservative 107; Mismatches 247; Indels 95; Gaps 14;

Qy 21 EQSRRNEGSHPSNQSQTTAQBENKGEKSLTKSTPTVSEPHNTIQLKSKNSG 80
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 38 EEKEEKEEKEEKEEKEEKEEVEKEEATNSTVPAKHEPQLQVED--TDADSG 94
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 81 DL-----TTNPDQNAEPGTGTVPEQKEMDGKGGPN-----SPONKPPAA 121
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 95 PLIPEETLPPERPSPVSKSDTLTVPGAAAAGHKKLPQSDDEAEELKALSPAPVA 154
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 122 ---PVINEYDAQ-----LHNVKRMQRORTALYKVKLVGDLSSPEAS 161
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 155 WSDPTTQEAQDQRAASTASQNSAINDRLOELVKMFKEKTEKVEKLIIDPDVTSDEES 214
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 162 PQAKPTAVPVKESDDKPT-----EHYRLLWFVKYKQKPLTEYLKRIKPLNSIDSYT 214
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 215 PKPS-PAKKAPEPDPAQPAEVAEAEHYYCDMLCKFKRPLKMY---RFQSIDPLT 269
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 215 DRVLLMLLVTLAYNNWCPIPLRVPYPTQANIHFWLADIICDIYLYDMLFQPR 274
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 270 NLMTYILMFFVLAWNNCMLIPVRWAPPYQADNIHFWLLMDYLCDFIYLLDITVFQMR 329
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 275 LQFVRGGDIIIVDSNELRHGVRTSTKFDLVASIIIPFDICYLFFGNPMFRANMLKYTSF 334
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 330 LQFVKGDDIITDKKEMRNLYLKSRRFMDLCLLPDLYLKLGNPLLRPLRCLKYNAF 389
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 335 PEFNHLESIMDKAYIVRITGTYLFIHLINACVYVWASNYEGIGTRVWYDGEENEY 394
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 390 PEFNRLAELLSKAYVYVIRITAYLLYSLHNSCLYVWASAFQIGSTHWYDVGNSY 449
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 395 LRCYIAVTRITITIGLPEPTLFEIVPQLNFFSGVVFSSLLIGQMRDVTGAATANQY 454
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 450 IRCYIYAVKTLITIGLPPDQTLFEIVPQLNFFYVGFVAFSVMIQMRDVVGAATAGTY 509
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 455 PRACMDTIAWNNYSPKLVOKVRVYETWDSQRMLEDSDLLKTLPTTVQLALADV 514
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 510 YRSCMDSTVKYMNFKIPRSQNVKVTWYETWHSQGMLEDSELMVQLPKOKRLDLADV 569
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :

515 NFSIISKVDLPFKGCDTQMIYDMLRLKSLVLYLPGDFVCKKGEIKEMVIIKHGEVQVLGG 574
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
570 NYSIVSKVALFQGCDDQMIYDMLRLKSLVLYLPGDFVCKKGEIKEMVIIKHGEVQVLGG 629
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
575 PDGTFKLVLTAKAGSVFGEISLLAAGGNGRRRTANVVAHGFANLLTLDKKTLOEILVHYVDS 634
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
630 PDGKAVLVLTAKAGSVFGEISLLAAGGNGRRRTANVVAHGFANLLTLDKKTLOEILVHYVDS 689
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
635 ERIIMKKARVLLKQAKTAEATPPRKDLALLFPKPEETPKLFTKLLGCTGKAS----- 687
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
690 QKLLRKKARRMLRNKK-----PKEEKSVLLLPRACTPKLFNAALAAAGWGPRGAKGG 744
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
688 -----LARLLKLKREQAA-----QKENSEGEGEGEGEKENEDKQENEDKX 734
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
745 KLAHLRARLAKELAAEAARQQQLLEQAKSSQEAAGGEGSGATDQAPQEP----- 795
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
735 KENEDKDKGREPEKPLDRPECTASPIAVSEEPHSVTRTVLPRTSRSQSLIISMAPSAG 794
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
796 PEPKDPKPPGPPPE-----PSAOSPPPPASAKPE--ESTGEAAGPPPEPSVRIVSPGDDP 848
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
795 GEEVLTIEVKEKAKQ 809
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
849 GEQTLSEVLEEKKE 863

RESULT 5
O35788 PRELIMINARY; PRT; 1339 AA.
ID AC O35788
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DN Cyclic nucleotide-gated channel beta subunit.
GN Name=CNG4.1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-Sprague-Dawley;
RA Sautter A., Biel M., Hofmann F.;
RT "Molecular cloning of cyclic nucleotide-gated cation channel subunits
RT from pineal gland.";
RL Mol. Brain Res. 47:171-175 (1997).
DR EMBL; AJ000496; CAA04133.1; -.
DR HSSP; O88703; 1043.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005216; P: ion channel activity; IEA.
DR GO; GO:0006811; P: ion transport; IEA.
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR005821; Ion Trans.
DR Pfam; PF00027; cNMP binding; 1.
DR Pfam; PF00520; Ion_trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; UNKNOWN_1.
DR PROSITE; PS00889; cNMP_BINDING_2; 1.
DR PROSITE; PS50042; cNMP_BINDING_3; 1.
DR PROSITE; PS50043; cNMP_BINDING_4; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 1339 AA; 151046 MW; FFAD64A6A81AB49A CRC64;

Query Match 46.3%; Score 1959; DB 2; Length 1339;
Best Local Similarity 46.3%; Pred. No. 1.8e-101;
Matches 400; Conservative 121; Mismatches 240; Indels 102; Gaps 15;

Qy 11 VKPIGENNENQSSRRNEGSHPSNQSQTTAQBENKGEKSLTKSTPTVSEPHNTIQ 70
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
512 IQLEPEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEE 568
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
71 DKLSKKNSSGDLTNPDPQN-----AAEPTGTVP-----EQKEMDPGK 108
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
569 DTAAGGLPIPETTIPPTPPPPVSPAKSDTLAVPSAATHRKKLPQSDDEAEELKALSPAE 628
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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QY 109 -----EGPNSPQ-----NKPPAAPVINEYADALHNLVKRMQRTALYKKKLAVE 152
Db 629 SPVVAWSDDPTTPOEADGEDRAASTASQNSAIIND----RLQELVKMFKERTEYKKEKLD 684
QY 153 GDLS-----SPASQOTAKPTAVPVK--ESDDKTEHYRLLWFKVKKMPLETEYVKRIKL 206
Db 685 PDVTSDEESPSPAKPADSPAKPAEAAEAEHHCYDMLCKCKFRKRPWKMY-----QF 740
QY 207 PMSIDSYDRLYLWLLVTLAYVNNCWFIPLRLVEPQVADNTHYMLADIICDIILY 266
Db 741 POSIDPLTNLYLWLFVVLAWNNCWLIIPVRWAFYQQRADNHLMLDYLCDIFYLL 800
QY 267 DMLFIQPLQVRGDDIIVDSNELRKHRYSTKFLQDVASIIIPDICYLFEGFNMPFRAN 326
Db 801 DITVQMLQFVKGDDIITDKEMRNLYKSQRKMDLLCLPLDLYLKLGNPLRLRP 860
QY 327 RMLKYTSFFPNHLESIMDKAYIRYVIRITGYLLFILHINACVYVWASVEGIGTRRW 386
Db 861 RCLYMAFFFNRLKLAISKAYVYVIRITAYLLYSLHNSCLYVWASAFQIGSTHW 920
QY 387 YDGGNEYLRCYVAVRTLITIGLBPQTLFEIVFOLLNFFSGVFVFSLLIGMRDVIG 446
Db 921 YDGVNSYIRCYVAVRTLITIGLBPQTLFEIVFOLLNFFSGVFVFSLLIGMRDVIG 980
QY 447 AATANQYFRACMDDTIAYMNNYSIPKLQKRVRTYETWDSQRMDESLDKLTLPTTV 506
Db 981 AATAGQTYRSCMDSTVKYMNFKYIPRSVQNRVKTWYETWHSQGMDESELVQLPDKM 1040
QY 507 QALALADVNSIISKVDLPFGCDTQMIYDMLRLKLSVLYLPDGPVCKKGHIGKMYIKH 566
Db 1041 RLDLADVNNYIVSKVALFGCDRQMIYDMLKRLSVVLYLPDGPVCKKGHIGKMYIKH 1100
QY 567 GEVQVLGGPDKTVLTKAGSVFGEISLLAAGGNRRRTANVAHGPNLTLDDKTLQE 626
Db 1101 GQVQVLGGPDKTVLTKAGSVFGEISLLAAGGNRRRTANVAHGPNLTLDDKTLQE 1160
QY 627 ILVHYPDSERILMKARVLLKQAKTAETPPRKDLALLPPKKEETPKLFTLLGGTGKA 686
Db 1161 ILVHYPDSERILMKARVLLKQAKTAETPPRKDLALLPPKKEETPKLFTLLGGTGKA 1215
QY 687 S-----LARLLKLKQAA-----QKENSEGEEGKENEKQKENEK 726
Db 1216 GPRGAKGKLAHLARLKLKQAA-----QKENSEGEEGKENEKQKENEK 1275
QY 727 QKENEKQKENEKQKENEKQKENEKQKENEKQKENEKQKENEKQKENEKQKENEK 786
Db 1276 -----EPKEPP--EPPAPSPPPASAKPEG--STEEAAGPEPSVRI 1313
QY 787 SMAPSAGGEBVTIEVKEKAKQ 809
Db 1314 RVSPGPDGQTLSEMLEBKE 1336

RESULT 6
O43636 PRELIMINARY; PRT; 1245 AA.
AC O43636;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rod photoreceptor CNG-channel beta subunit.
GN Name=RCNC2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Grunwald M.E., Yu W.P., Yu H.H., Yau K.W.;
RT "Identification of a domain on the beta subunit of the rod cGMP-gated
RT cation channel that mediates inhibition by calcium-calmodulin.";
RL J. Biol. Chem. 0:0:0(1998).
DR EMBL; AF042498; AAC04830.1; -.

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DR PIR; S32538; S32538.
DR PIR; S69275; S69275.
DR HSSP; O88703; IQ43.
DR GO; GO:0015276; Filigand-gated ion channel activity; TAS.
DR GO; GO:0006810; P:transport; TAS.
DR GO; GO:0007601; P:visual perception; TAS.
DR InterPro; IPR000595; CNMP binding.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel_pore.
DR Pfam; PF00027; CNMP_binding; 1.
DR Pfam; PF00520; Ion_trans; 1.
DR SMART; SM00100; CNMP; 1.
DR PROSITE; PS00888; CNMP_BINDING_1; UNKNOWN_1.
DR PROSITE; PS00889; CNMP_BINDING_2; 1.
DR PROSITE; PS00442; CNMP_BINDING_3; 1.
KW Ion transport; Ionic channel; Receptor; Transmembrane; Transport.
SQ SEQUENCE 1245 AA; 139159 MW; 40C4860BFCF86126 CRC64;

Query Match 46.1%; Score 1952; DB 2; Length 1245;
Best Local Similarity 46.4%; Pred. No. 4.1e-101;
Matches 405; Conservative 121; Mismatches 237; Indels 110; Gaps 18;

QY 14 IGENNENQSSRRNEBEGSHPSNQSQOTTAQE--ENKGE---EKSLTKTPTVTSBPHYN 68
Db 403 VGEEAKKEAEKAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAE 462
QY 69 IQDK-----LSKNSSGDLTNPDPQNAAEPTGTVPEQKEMDPKEGPN----- 112
Db 463 VEDTDADSCPLMAEENPPS--TVLPPSPAKSDTLIVPSSASGTHRKKLPSEDEAEELK 520
QY 113 --SPQNKP-----PAAP-----VINEYADAQLHNLVKRMQRTALY 146
Db 521 ALSPAESPVVAWSDDPTTPOEADGEDRAASTASQNSAIIND----RLQELVKLFKERTKV 576
QY 147 KKKLVEGDL-----SPEASQOTAKPTAVPVKESDDKPT--RHYRLLMFKVKKMPLEBY 200
Db 577 KEKLDIPDVTDESPKPSKPAKPAEPADTKPAEAEVPEEHEHYCDMLCKCKRHPWKY 636
QY 201 LKRIKLPSIDSYDRLYLWLLVTLAYVNNCWFIPLRLVEPQVADNTHYMLADIIC 260
Db 637 ----QFPQSIDPLTNLYLWLFVVLAWNNCWLIIPVRWAFYQQRADNHLMLDYL 692
QY 261 DIILYDMLFIQPLQVRGDDIIVDSNELRKHRYSTKFLQDVASIIIPDICYLFEGFN 320
Db 693 DLIIYFLDITVFTQLQVRGDDIITDKDMRNLYKSRRFKMDLLSLLPLDLYLKVGVN 752
QY 321 PMFRANRMLKYTSFFPNHLESIMDKAYIRYVIRITGYLLFILHINACVYVWASVEGI 380
Db 753 PLLRLPRLCKYMAFFFNRLKLAISKAYVYVIRITAYLLYSLHNSCLYVWASAYQGL 812
QY 381 GTTRWYVDGEGNEYLRCYVAVRTLITIGLBPQTLFEIVFOLLNFFSGVFVFSLLIGQ 440
Db 813 GSTHWYDGVNSYIRCYVAVRTLITIGLBPQTLFEIVFOLLNFFSGVFVFSLLIGQ 872
QY 441 MEDVIGAATANQYFRACMDDTIAYMNNYSIPKLQKRVRTYETWDSQRMDESLDK 500
Db 873 MEDVIGAATAGQTYRSCMDSTVKYMNFKYIPRSVQNRVKTWYETWHSQGMDESELV 932
QY 501 TLPTTVQALALADVNSIISKVDLPFGCDTQMIYDMLRLKLSVLYLPDGPVCKKGHIGKE 560
Db 933 QLPDKMRLDLAIDVNNYIVSKVALFGCDRQMIYDMLKRLSVVLYLPDGPVCKKGHIGRE 992
QY 561 MYIIKHGEVQVLGGPDKTVLTKAGSVFGEISLLAAGGNRRRTANVAHGPNLTLDD 620
Db 993 MYIIQAGQVQLGGPDKTVLTKAGSVFGEISLLAAGGNRRRTANVAHGPNLTLDD 1052
QY 621 KKTLEIILVHYPDSERILMKARVLLKQAKTAETPPRKDLALLPPKKEETPKLFTLL 680
Db 1053 KKDLEIILVHYPDSERILMKARVLLKQAKTAETPPRKDLALLPPKKEETPKLFTLL 1107
QY 681 GGTGKAS-----LARLLKLKQAA-----QKENSEGEEGKENEKQKENEK 728
Db 1108 AMTGKGGKAGKGLAHLARLKLKQAA-----QKENSEGEEGKENEKQKENEK 1164

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Db	829	DQTHPKAATDPAPRTPEPP-GSPSPSPASLGSCGEEGPAEPESHSVR-----	882	QY	113	--SPQKP-----PAAP-----	VINEYADAQLHNLVKRMORTALY	146
QY	777	RGTSRQSLIISMAPSAGGEEVLTIEVKEKAKQ	809	Db	527	ALSPAESPVVANSDDPTPKDQDQRAASTNSAIIND-----	RLQELVKLFKERTKV	582
Db	883	-----ICMSGPGEPGQILSVKMPEREE	906	QY	147	KKLVEGDLS-----SPEASPTAKTAVPPVKSDDKPT--	EHYRLLMFKVKGMPLTEY	200
				Db	583	KEKLDIDPVTSDSESPKSPAKKAPAPDTPKPAEAPVEEHEHYCDMLCKFKHRPWKY		642
RESULT 8				QY	201	LKRIKLPNSIDSVTDLRYLLWLLVTLAYNWCWFIPILSLVPPYQADNHHVWLIADIIC		260
Q9UMG2				Db	643	-----QFPQSIDPLTNLMYVWLFVVMAMWNCWLPVWPAFPYQTPDNIHHLMDYLC		698
AC	Q9UMG2			QY	261	DIYLYDMLFIQRLQFVRGGDIIVDSNELRKHRTSTKQFQDVASIIPDICYLFFGFN		320
DT	01-MAY-2000	(TREMBlrel. 13, Created)		Db	699	DLIYFLDITVFQTRLQFVRGGDIITDKDMRNLYLKSRRFKMDLLSLPLDLFLYLVKGVN		758
DT	01-MAR-2004	(TREMBlrel. 26, Last annotation update)		QY	321	PMFRANRMLKYTSFPEFNHLESIMDKAYIVRTTGYLLFILHINACVYVWASNYEGI		380
DE	CGMP-gated cation channel beta subunit.			Db	759	PLLRPRCLUKYMAFPEFNSRLESILSKAYVYVIRKTYAYLLYSLHNSCLYYWASAYQGL		818
GN	Name=CNCG2;			QY	381	GTRWVYDCEGNEYLCRYVAVRTLITIGLPEPOTLFEIVFQLLNFFGVFVFFSLIGQ		440
OS	Homo sapiens (Human).			Db	819	GSTHWYDVGNSYIRCYFAVKTLITIGLFPDKLFEIVFQLLNFFGVFVFFSLIGQ		878
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			QY	441	MRDVGAATANQNYFRACMDDTIAYNNYSIPKLQKRVRTWYETWDSQRMLEDLLK		500
OC	Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.			Db	879	MRDVGAATAGQTYVRSMDSTVKYMNFKYIPKSVQNRVKTWYETWDSQRMLEDLLK		938
OX	NCBI_TaxID=9606;			QY	501	TLPTVOLALADVNFSIISKVDLPKGDCTQIMYDMLLKSIVLYLPGDFVCKKGIGKE		560
RN	[1]			Db	939	QLPDKMRLDAIDVNYNIVSKVALPGQCDRQIMFDMLKELRSVYVLPNDYVCKKGIGRE		998
RP	SEQUENCE FROM N.A.			QY	561	MYIHKHGEVVLGGPDGTVLTKAGSVFGISLLAAGGNNRTANVAHGFANLLTLD		620
RC	TISSUE=Retina;			Db	999	MYIHKHGEVVLGGPDGTVLTKAGSVFGISLLAAGGNNRTANVAHGFANLLTLD		1058
RX	MEDLINE=96070429; PubMed=7590744;			QY	621	KKTQELVHPDSEIRILMKARVLLKQKATAEATPPRKDLALLFPKKEETPKLFTLL		680
RA	Ardeil M.D., Makhiya A.K., Oliveira L., Miniou P.,			Db	1059	KKDLNEILVHPDESQKLRLKARRMLRSNNK-----PKEKSVLILPPRAGTPKLFAAL		1113
RA	Viegas-Pequignot E., Pittler S.J.;			QY	681	GGTGKAS-----LAEILLKREQAQKENSEGEEGKENEKQENEDKQK		728
RT	"cDNA, gene structure, and chromosomal localization of human GARI			Db	1114	AMTGKMGKGAGKGLAHLRLAKSLAALAAKHEEL---VEQAKSODVKEEGSAAP		1170
RT	(CNCG3L), a homolog of the third subunit of bovine photoreceptor CGMP-			QY	729	ENEDKGE-NEKDQGRPEPEKPLDRPECTASPIAV-----EPEHSVRRTVLP		776
RT	gated channel.";			Db	1171	DQTHPKAATDPAPRTPEPP-GSPSPSPASLGSCGEEGPAEPESHSVR-----		1224
RL	Genomics 28:32-38(1995).			QY	777	RTSRQSLIISMAPSAGGEEVLTIEVKEKAKQ		809
RL	[2]			Db	1225	-----ICMSGPGEPGQILSVKMPEREE		1248
RP	SEQUENCE FROM N.A.			RESULT 9				
RC	TISSUE=Retina;			OS5157		PRELIMINARY;	PRT;	858 AA.
RX	MEDLINE=96338110; PubMed=8766832; DOI=10.1016/0014-5793(96)00588-1;			AC	OS5157;			
RA	Ardeil M.D., Aragon I., Oliveira L., Porche G.E., Burke E.,			DT	01-JUN-1998	(TREMBlrel. 06, Created)		
RA	Pittler S.J.;			DT	01-JUN-1998	(TREMBlrel. 06, Last sequence update)		
RT	"The beta subunit of human rod photoreceptor CGMP-gated cation channel			DE	05-JUL-2004	(TREMBlrel. 27, Last annotation update)		
RL	FEBS Lett 389:213-218(1996).			DE	Cyclic nucleotide-gated cation channel beta subunit (Cyclic			
RL	ENBL; U58837; AAB63387.1; --			DE	nucleotide-gated channel beta subunit 1b).			
DR	PIR; S69275; S69275.			GN	Name=CNCG4.3;			
DR	HSSP; O88703; IQ43.			OS	Rattus norvegicus (Rat).			
DR	Genew; HGNC:2151; CNGB1.			OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
DR	GO; GO:0016021; C:integral to membrane; IEA.			OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
DR	GO; GO:0005216; F:ion channel activity; IEA.			OX	NCBI_TaxID=10116;			
DR	GO; GO:0005267; F:potassium channel activity; IEA.			RN	[1]			
DR	GO; GO:0006811; P:ion transport; IEA.			RP	SEQUENCE FROM N.A.			
DR	GO; GO:0006813; P:potassium ion transport; IEA.			RC	STRAIN=Sprague-Dawley; TISSUE=Olfactory epithelium;			
DR	InterPro; IPR005821; Ion Trans.			RX	MEDLINE=98208604; PubMed=9539801; DOI=10.1073/pnas.95.8.4696;			
DR	InterPro; IPR001622; K+channel_pore.			RA	Sauter A., Zong X., Hofmann F., Biel M.			
DR	Pfam; PF00027; CNMP_binding; 1.			RT	"An isoform of the rod photoreceptor cyclic nucleotide-gated channel			
DR	Pfam; PF00520; Ion_trans; 1.							
DR	SMART; SM00100; CNMP; 1.							
DR	PROSITE; PS00888; CNMP_BINDING_1; UNKNOWN_1.							
DR	PROSITE; PS00889; CNMP_BINDING_2; 1.							
DR	PROSITE; PS50042; CNMP_BINDING_3; 1.							
KW	Ion transport; Ionic channel; Transmembrane; Transport.							
SQ	SEQUENCE 1251 AA; 139604 MW; 4701C53DB13C9055 CRC64;							
	Query Match							
	Best Local Similarity							
	Matches 403; Conservative 122; Mismatches 238; Indels 110; Gaps 18;							
QY	14	IGNNENQSRNRNEGSHPSNQSQTQAE--ENKGE---EKSLTKSTPTVTSSEPHYN	68					
Db	409	VGEAKKEAEKAEAEVAEEAEKEPQDWAETKEEPEAEAEAAASGGVPATKQHPVQ	468					
QY	69	IQDK-----LSKKNSSGLTTNPPQNAAEPTGTVPQEKMDPKGPN-----	112					
Db	469	VEUTDADSCPLMAEENPPS--TVLPSPSPAKSDTLVPSASGTHRRKLPSEDDAEELK	526					



beta subunit expressed in olfactory neurons.";  
Proc. Natl. Acad. Sci. U.S.A. 95:4696-4701(1998).  
[2]  
RN MEDLINE=99307326; PubMed=10377344;  
RX Bonigk W., Bradley J., Muller F., Sesti F., Boekhoff I., Ronnett G.V.,  
RA Kaupp U.B., Frings S.;  
RA "The native rat olfactory cyclic nucleotide-gated channel is composed  
RT of three distinct subunits.";  
RT J. Neurosci. 19:5332-5347(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Boenigk W., Sesti F., Bradley J., Ronnett G., Mueller F., Kaupp U.B.,  
RA Frings S.;  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ000515; CAA04152.1; -;  
DR EMBL; AF068572; AAC19120.1; -;  
DR HSSP; O88703; 1043.  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR GO; GO:0005216; P: ion channel activity; IEA.  
DR GO; GO:0006811; P: ion transport; IEA.  
DR InterPro; IPR000595; cNMP binding.  
DR InterPro; IPR005821; Ion trans.  
DR Pfam; PF00027; cNMP binding; 1.  
DR Pfam; PF00520; Ion trans; 1.  
DR SMART; SM00100; cNMP; 1.  
DR PROSITE; PS00888; cNMP BINDING 1; UNKNOWN\_1.  
DR PROSITE; PS00889; cNMP BINDING\_2; 1.  
DR PROSITE; PS00442; cNMP BINDING\_3; 1.  
DR Ion transport; Ionic channel; Transmembrane; Transport.  
KW SEQUENCE 858 AA; 96358 MW; 10B07CC41119F9A4 CRC64;  
Query Match 45.4%; Score 1923; DB 2; Length 858;  
Best Local Similarity 47.3%; Pred. No. 1.le-99;  
Matches 396; Conservative 114; Mismatches 228; Indels 100; Gaps 15;  
Qy 37 SQQTAAQENKGER-KSLKTKSTPTVTSSEPTNIQDKLSKNSGDLTNPQPQN-----90  
Db 53 SRRTALNSNFTKEIRSRRLVPATKEHPDELQVEDTDAEAGLPIPETIIPPPVSP 112  
Qy 91 AAETGTVP-----EKKMDPGK-----EGNSPQ-----NK 117  
Db 113 AKSDTLAVPSAATHRKKLPSQDDAEELKALSPAESPVVMSDPTTPQBADGEDRAASTA 172  
Qy 118 PPAAPVINEYADAQHLNLRKMRQRTALYKKKLVEGDL-----SPASPTAKPTAVRPV 173  
Db 173 QNSAIIND-----RLQELVGNFKERTEKVAKEKIDPDVTSDEESPKSPAKKAPASPAQ 228  
Qy 174 K--ESDDKPTHEYRLLFVKVKKMPLTEYLKRIKLPSNIDSYDRLYLWLLLVLTAYNW 231  
Db 229 KPAEAAEAEHEDYCDMLCKKRPWKY----QFPQSIDPLTNLWLLFVVLANNW 284  
Qy 232 NCWFIPLRVFPYQTADNIHWLIADIICDIYLYDMLFIQPLQVRGSDIIVDSNEUR 291  
Db 285 NCWLIPLVRWAFPYQRADNIHLWLLMDYLCDFIYLLDITVFMQLQVRGSDIITDKENR 344  
Qy 292 KHYRTSKFOLDVASIIPEDICYLFFGFMFRANMLKYTSFERNHLESIMDKAYIT 351  
Db 345 NNYLKSQRKMDLCLLPLDFLKLGVNPLLPCLTKTMAFFFNKNLEAILSKAYY 404  
Qy 352 RVIRTTGYLLFILHNAVCYYWASNYEGIGTTRWYDGEENEYLRICYWAVRTLTIGL 411  
Db 405 RVIRTTAYLLSLHNSCLYYWASAFQIGSTHWYDGVNSYIRCYWAVKTLTIGL 464  
Qy 412 PEPOTLFEIVPQLNFPFSGVVFSSLIGQMRDVI GAATANQNYFRACMDDTIAYWNYSI 471  
Db 465 PDPOTLFEIVFQLNLYETGVFAFSVMIGQMRDVVGAATAGQTYRSCMDSTVKYNFYKI 524  
Qy 472 PKLVOKERVTRYETWDSQRMLESLLKTLPTTVQLALADVNFISIISKVDLPKGDCTQ 531  
Db 525 PRSQNVKVKTYEYTHWSQGMDESELMVQLPDKMLDLADVNYNIVSKVALFOGCDRQ 584  
Qy 532 MIYDMLRLKLSVLYLPDGFCKEIGEKENYIIKHGEVVOVLGGPDGKTVLVLTKAGSVFG 591





RC TISSUE=Retina;  
RA PubMed=2014230;  
RX Sugimoto Y., Yatsunami K., Tadjimoto M., Khorana H.G., Ichikawa A.;  
RT "the amino acid sequence of a glutamic acid-rich protein from bovine  
RL retina as deduced from the cDNA sequence";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:3116-3119(1991).  
CC -|- SUBUNIT: Forms functional heterooligomeric channels with CNG3.  
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -|- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Comment=Isoform CNG4D is the most frequent isoform  
CC (CNG4D:CNG4C:CNG4E = 20:2:1) in testis;  
CC Name=CNG4C;  
CC IsoId=Q28181-1; Sequence=Displayed;  
CC Name=CNG4D;  
CC IsoId=Q28181-2; Sequence=VSP\_001109;  
CC Name=CNG4E;  
CC IsoId=Q28181-3; Sequence=VSP\_001108;  
CC -|- TISSUE SPECIFICITY: Retina, testis, kidney, heart and brain.  
CC -|- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel  
CC (TC 1.A.1.5) family.  
CC -|- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.  
CC  
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CC  
CC -----  
CC EMBL; X89626; CAA61769.1; -;  
CC EMBL; X94707; CAA64367.1; -;  
CC EMBL; M61185; AAA30536.1; -;  
CC PIR; A40437; A40437.  
CC Reactome; Q28181; -;  
CC InterPro; IPR000595; cNMP binding.  
CC InterPro; IPR005821; Ion Trans.  
CC Pfam; PF00027; cNMP binding; 1.  
CC Pfam; PF00520; Ion Trans; 1.  
CC PROSITE; PS00888; CNMP BINDING\_1; 1.  
CC PROSITE; PS00889; CNMP BINDING\_2; 1.  
CC PROSITE; PS50042; CNMP BINDING\_3; 1.  
CC Alternative splicing; cAMP-binding; Direct protein sequencing;  
KW Ion transport; Ionic channel; Multigene family; Transmembrane.  
FT CHAIN 1 590 Glutamic acid-rich protein.  
FT CHAIN 454 1394 Cyclic-nucleotide-gated cation channel 4.  
FT DOMAIN 1 770 Cytoplasmic (Potential).  
FT TRANSMEM 771 789 H1 (Potential).  
FT DOMAIN 790 803 Extracellular (Potential).  
FT TRANSMEM 804 822 H2 (Potential).  
FT DOMAIN 823 847 Cytoplasmic (Potential).  
FT TRANSMEM 848 867 H3 (Potential).  
FT DOMAIN 868 904 Extracellular (Potential).  
FT TRANSMEM 905 927 H4 (Potential).  
FT DOMAIN 928 971 Cytoplasmic (Potential).  
FT TRANSMEM 972 991 H5 (Potential).  
FT DOMAIN 992 1075 Extracellular (Potential).  
FT TRANSMEM 1076 1096 H6 (Potential).  
FT DOMAIN 1097 1394 Cytoplasmic (Potential).  
FT NP BIND 1084 1222 cAMP (by similarity).  
FT BINDING 1144 1144 cAMP (Potential).  
FT BINDING 1156 1156 cAMP (Potential).  
FT CARBOHYD 1067 1067 N-linked (GlcNAc...) (Potential).  
FT VARSPIC 515 532 Missing (in isoform CNG4E).  
FT VARSPIC 522 530 /FtId=VSP\_001108.  
FT VARSPIC 530 530 Missing (in isoform CNG4D).  
FT VARSPIC 530 530 /FtId=VSP\_001109.  
FT CONFLICT 341 341 K -> E (in Ref. 3).  
FT CONFLICT 454 465 REEEDEERED -> MRAGQGRC (in Ref. 2).  
FT CONFLICT 482 482 R -> Q (in Ref. 2 and 3).  
FT CONFLICT 499 499 A -> T (in Ref. 3).  
FT CONFLICT 572 590 VPATEBHEPELQVEDADADS -> GSFQMSFPEALQCEALK

FT CONFLICT 1283 1283 R (in Ref. 3).  
FT CONFLICT 1289 1289 S -> A (in Ref. 2).  
FT CONFLICT 1336 1336 R -> A (in Ref. 2).  
FT CONFLICT 1338 1338 D -> E (in Ref. 2).  
SQ SEQUENCE 1394 AA; 155064 MW; EE6DA559BE3744A7 CRC64;  
Query Match 45.3%; Score 1920; DB 1; Length 1394;  
Best Local Similarity 45.9%; Pred. No. 3e-99;  
Matches 401; Conservative 118; Mismatches 242; Indels 112; Gaps 17;  
QY 15 GENNENEQSSRRNEBSPHSNQSQTAAQENKGBEKSILKTSPTVTSBEPHTNIQDK-- 72  
Db GAQAQGEVGAQEQDGVGGA-QDQSTSHQELQ--EALADSSGVGPATEBHEPELQVEDADA 588  
QY 73 -----LSKKNSSGDLTTNPDQNAAEPTGTVP-----BQKENDPGK 108  
Db DSRPLIAEENPPSPVQLPLSP--AKSDTLAVPGSATGSRKLRLPSODDABAEELKMLSPAA 646  
QY 109 -----EGNPSQNKPPA-----APVINEVADAQHLNFKRMORTALYKKKLVE 152  
Db SPVAVMSDFTSQGTDDQDRATSTASONSAILND-----RLQELVKLFKERTKVKELID 702  
QY 153 GDLS-----SPEASPTAKPTAVPPVK--ESDDKPTHEYRLLWFKVKMPLTEYLKRIK 206  
Db PDVTSDESPKPSPAKAPAPAEVAPAGOVEEHCMLCKCFKRRPWKKY-----QF 758  
QY 207 PHSIDSYDRLYLLMLLLVTLAVNNCWFIPLRLVFPYQTDNIHVMYLIADIIICDIILY 266  
Db POSIDPLTNMLYLLMLFFVLLANNWNCWLIPLVRAPFYQTPDNHJLMLDYLCDIILY 818  
QY 267 DMLFTQPRLOFVRGDIIVDSNELRKHRTSTKFDLVAISIIPDICYLFFGFNPMFRAN 326  
Db DITVFQMRLOFVRGDIITDKKEMNNYVKSQRFKMDMLCLPLDLLLYLKFGVNPRLRP 878  
QY 327 RMLKTSPEFNNHLESIMDKAYIVRVITRTGYLLFILHINACVYVWANYEGIGTRWV 386  
Db RCLKYMAFPEFNNRLESILSKAYVYRVITRTAYLLYSLHNSCLYVWASAYEGLGTHWV 938  
QY 387 YDGEQNEVLYCYVWAVRTLTITIGLPEOTLFEIVFOLLNFFSGVVFSSLLQMEDVLG 446  
Db YDGVGNSYIRCYVWAVKTLITITIGLPPDRLFEIVFQGLNYFTGVFAFVLMQMDRVVG 998  
QY 447 AATANQVFRACWDDTIATMNNYSIPKLQKQVRYWYETWDSQRMDESLLKLTPTV 506  
Db AATAGTYRSCWDSIVKYMNFYKIPRSVQNVKTYEYTHWSQGMDESELVQLPDKM 1058  
QY 507 QALALDVNFSIISKVDLPKGCOTQMIYDMLRLKSVLYLPGDFVCKGGEIKEMYIIKH 566  
Db RLDLAIDVNSYISVSKVALFQGCDDQWIFDMLKRLRSVVYLPNDYVCKGGEIGREMYIIQA 1118  
QY 567 GEVOVLGGPDGTVLVTLKAGSVFGEISLLAAGGNRRRTANVAHGFANLLTLDKKTQES 626  
Db GQVOVLGGPDGKSVLYTLKAGSVFGEISLLAAGGNRRRTANVAHGFNTLFLDKKDLNE 1178  
QY 627 ILVHPDSEIRILMKARVLLKQAKTAEATPPRKDLALFPKKEPTPKLFTLLGGTGKA 686  
Db ILVHPESQKLRLKARMLRNNK-----PKEKSVLILPPRAGTPKLFNLAALAAAGKM 1232  
QY 687 SL-----ARLLKLRQAAQKENSEGGEKEKEDKQKEDKQKEDKQKEDKQKEDK 734  
Db GAKGGGGRGLALLRLARLKEALAAEAARQQQL---LEQAKSEDAARVGE-----G 1280  
QY 735 KENEDKDKGREPEEKPLDRPECTA-----SPTAVEEHPHVRVTRVLP 776  
Db SASPQPPRPEPEAPAEPAPEPTAPEPLAPEAPAEAPAPSSPPSPASQRPBGDKDAAP 1340  
QY 777 RGTSRQSLIISMAPSAEGGEEVLTIEVKEKAKQ 809  
Db ---EEHPVRIHVTGLGDPSEQLLVEVPEKQEE 1370  
RESULT 14

Q9W2D5 Q9W2D5 PRELIMINARY; PRT; 1040 AA.  
AC Q9W2D5; Q8IH43;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DE 25-OCT-2004 (TRENBLrel. 28, Last annotation update)  
DE Q9W2D5-PA (GH25102p).  
GN ORFNames=CG17922;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_taxid=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA Sutton G.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Bugan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista A.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fodor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Hadravsky N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hoatin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskens D.R., Pacle J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J.J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster."  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstock G., Scherter S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila  
melanogaster euchromatic genome sequence."  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirkas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the Drosophila melanogaster euchromatin:

a genomics perspective.";  
RT Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Ruso S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
systematic review."  
RT Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RX FlyBase;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkley;  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
RA Miranda A., Mungall C.J., Nunoo J., Pacle J., Paragas V., Park S.,  
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
RA Celniker S.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003454; AAF46757.2; -  
DR EMBL; BT001439; AAN71194.1; -  
DR HSPF; 088703; IQ3E.  
DR FlyBase; FBgn0034656; CG17922.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005216; P:ion channel activity; IEA.  
DR GO; GO:0005267; P:potassium channel activity; IEA.  
DR GO; GO:0006811; P:ion transport; IEA.  
DR GO; GO:0006813; P:potassium ion transport; IEA.  
DR InterPro; IPR005821; Ion Trans.  
DR InterPro; IPR001622; K-channel\_pore.  
DR Pfam; PF00027; cNMP binding; 1.  
DR Pfam; PF00520; Ion\_trans; 1.  
DR SMART; SM00100; cNMP; 1.  
DR PROSITE; PS00889; cNMP\_BINDING\_1; UNKNOWN\_1.  
DR PROSITE; PS00889; cNMP\_BINDING\_2; UNKNOWN\_1.  
DR PROSITE; PS00442; cNMP\_BINDING\_3; 1.  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 27, 2005, 03:59:35 ; Search time 10099 Seconds  
(without alignments)  
11659.191 Million cell updates/sec

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sta.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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3	1682.2	69.2	2826 4 AF490511 Canis fam
4	1362.4	56.1	4710 10 MMU243572
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6	577.4	23.8	3025 9 HUMCNGCCB
7	577.4	23.8	3408 9 HUMCNGCCA
8	577.4	23.8	4033 9 HSU58837
9	577.4	23.8	4382 9 AF042498 Homo sapi
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11	575.2	23.7	4763 10 BC045114
12	572.2	23.5	3083 4 AF074012
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18	568	23.4	3236 6 CQ880122
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21	330	13.6	205816	9	AC013751	AC013751 Homo sapi
22	237.4	9.8	2511	3	CEU73476	U73476 Caenorhabdi
23	223	9.2	3275	6	CQ598668	CQ598668 Sequence
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25	217.8	9.0	3099	10	BC046523	BC046523 Mus muscu
26	196.2	8.1	441	10	AF015728	AF015728 Rattus no
27	187.4	7.7	1709	3	AY060725	AY060725 Drosophil
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38	166.4	6.8	2297	10	MMU19717	U19717 Mus musculu
39	164.8	6.8	2474	10	MUSCNGC	M84742 Mus musculu
40	162.4	6.7	6312	3	AF091302	AF091302 Limulus p
41	161.4	6.6	58409	10	AL772281	AL772281 Mouse DNA
42	155.6	6.4	2612	5	GRODCNG	X89599 G.gallus mR
43	155.4	6.4	68732	2	AC151330	AC151330 Xenopus t
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ALIGNMENTS

RESULT 1	AF272900	Homo sapiens cone photoreceptor cyclic nucleotide-gated channel	4369 bp mRNA linear PRI 29-AUG-2000
LOCUS	AF272900		
DEFINITION	Homo sapiens cone photoreceptor cyclic nucleotide-gated channel		
ACCESSION	AF272900		
VERSION	AF272900.1	GI:9247065	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 4369)		
AUTHORS	Kohl, S., Baumann, B., Broghammer, M., Jagle, H., Sieving, P., Kellner, U., Spegal, R., Anastasi, M., Zrenner, E., Sharpe, L.T. and Wissinger, B.		
TITLE	Mutations in the CNGB3 gene encoding the beta-subunit of the cone photoreceptor cGMP-gated channel are responsible for achromatopsia (ACHM3) linked to chromosome 8q21		
JOURNAL	Hum. Mol. Genet. 9 (14), 2107-2116 (2000)		
MEDLINE	20414632		
PUBMED	10958649		
REFERENCE	2 (bases 1 to 4369)		
AUTHORS	Wissinger, B. and Kohl, S.		
TITLE	Direct Submission		
JOURNAL	Submitted (30-MAY-2000) University Eye Hospital, Molecular Genetics Laboratory, Auf der Morgenstelle 15, Tuebingen D-72076, Germany		
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ORIGIN

Query Match 100.0%; Score 2430; DB 9; Length 4369;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	167	ACAGCAG	226
QY	181	ACGTCTGAG	240
DB	227	ACGTCTGAG	286
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DB	347	CAG	406
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DB	407	GCTCTGTTTAAATGAGTATGCGATGCGGACGCTACAACTGGAAGAGAGAGAGAGAGAG	466
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QY	541	ACAG	600
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QY	601	TTAAAGGAG	660
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QY	661	TGCGCTCTGCTGCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	720
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RESULT 2
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DEFINITION Homo sapiens cone photoreceptor cGMP-gated cation channel
beta-subunit (CNGB3) mRNA, complete cds.
ACCESSION AF228520
VERSION AF228520.1 GI:8943947
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Sundin,O.H., Yang,J.M., Li,Y., Zhu,D., Hurd,J.N., Mitchell,T.N.,
Silva,E.D. and Maumenee,I.H.
Genetic basis of total colourblindness among the Pingelapese
islanders
JOURNAL Nat. Genet. 25 (3), 289-293 (2000)
MEDLINE 20347712
PUBMED 1088875
REFERENCE 2 (bases 1 to 2135)
Sundin,O.H., Yang,J.-M., Li,Y., Zhu,D., Silva,E.D. and
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1420	Qy	CTTGTGCAAAAGCCAGTTTCGGACTTTGTTATGAAATATACATGGGACTCTCAAGAATGCTA	1479
1081	Db	CTTGTGCAAAAGCCAGTTTCGGACTTTGTTATGAAATATACATGGGACTCTCAAGAATGCTA	1140
1480	Qy	GATGAGTCTGATTTTGTCTTAAGACCCCTACCAACTACGGTCCAGTTAGCCCTCGCCATTGAT	1539
1141	Db	GATGAGTCTGATTTTGTCTTAAGACCCCTACCAACTACGGTCCAGTTAGCCCTCGCCATTGAT	1200
1540	Qy	GTGAACCTTCAGCATCATCAGCAAAAGTCGACTTTGTTCAAGGGTTGTGATACAGATGATT	1599
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1600	Qy	TATGACATGTTCTTAAGCATTTGAATTCGGTCTCTATTTTGCCTGGTGACTTTGTCGAAA	1659
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1660	Qy	AAGGGAGAAATTTGGCAAGGAATTTATATCATCAAGCATGGAGAAGTCTCAAGTTCTTGGA	1719
1321	Db	AAGGGAGAAATTTGGCAAGGAATTTATATCATCAAGCATGGAGAAGTCTCAAGTTCTTGGA	1380
1720	Qy	GGCCCTGATGGTACTAAAGTTCTGGTTTACTCTCGAAGCTGGGTGGGTGTTTGAGAAATC	1779
1381	Db	GGCCCTGATGGTACTAAAGTTCTGGTTTACTCTCGAAGCTGGGTGGGTGTTTGAGAAATC	1427
1780	Qy	AGCCTTCTACGACGAGGAGGAAACCGTCGAACTGCCAATCTGTTGGGCCACCGGTTT	1839
1428	Db	--CCTTCTAGCAGCAGGAGGAAACCGTCGAACTGCCAATCTGTTGGGCCACCGGTTT	1485
1840	Qy	GCCAACTTTTAACTCTTAGACAAAAGACCCCTCCAAAGAAATTTCTAGTGCATTATCCAGAT	1899
1486	Db	GCCAACTTTTAACTCTTAGACAAAAGACCCCTCCAAAGAAATTTCTAGTGCATTATCCAGAT	1545
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1546	Db	TCTGAAAGGATCTCATGAAAGAAAGCCAGAGTGTCTTTTAAAGCAGAAGGCTAAGACCGCA	1605
1960	Qy	GAAGCAACCCCTCCAGAAAAGATCTTGCCCTCTTCCACCGAAGAGAGACACCC	2019
1606	Db	GAAGCAACCCCTCCAGAAAAGATCTTGCCCTCTTCCACCGAAGAGAGACACCC	1665
2020	Qy	AAACTGTTTTAAAACTCTCTTAGGAGGCAAGGAAAAAGCAAGTCTTCAAGACTACTCAAA	2079
1666	Db	AAACTGTTTTAAAACTCTCTTAGGAGGCAAGGAAAAAGCAAGTCTTCAAGACTACTCAAA	1725
2080	Qy	TTGAACGAGCAAGCAGCTCAGAGAAAGAAAAATTTCTGAAGGAGGAGAGGAAGAAGA	2139
1726	Db	TTGAACGAGCAAGCAGCTCAGAGAAAGAAAAATTTCTGAAGGAGGAGAGGAAGAAGA	1785

QY	2140	AAGAAATGAAATGAACAAAAAAGAAAATGAAGATAAACAAAAAGAAAATGAAGATAAA	2199
Db	1786	AAAGAAAATGAAGATAAACAAAAAAGAAAATGAAGATAAACAAAAAAGAAAATGAAGATAAA	1845
QY	2200	GGAAGAANAATCAAGATAAGATAAGGAGAGAGCCAGAGAGAGCCACTGGACAGA	2259
Db	1846	GGAAGAANAATGAAGATAAGATAAGGAGAGAGCCAGAGAGAGCCACTGGACAGA	1905
QY	2260	CCTGAATGTACACAAGTCTATTTCAGTGGAGAGAAACCCCACCTCAGTTAGAAAGACA	2319
Db	1906	CCTGAATGTACACAAGTCTATTTCAGTGGAGAGAAACCCCACCTCAGTTAGAAAGACA	1965
QY	2320	GTTTTACCAGAGAGGACTTCTCGTCAATCACTCATTTATCAGCATGCCTCTTCTGCTGAG	2379
Db	1966	GTTTTACCAGAGAGGACTTCTCGTCAATCACTCATTTATCAGCATGCCTCTTCTGCTGAG	2025
QY	2380	GCGGAGAGAGAGTCTTACTATTGTAAGTCAAAGAAAGGCTTAAGCAATAA	2430
Db	2026	GCGGAGAGAGAGTCTTACTATTGTAAGTCAAAGAAAGGCTTAAGCAATAA	2076
RESULT 3			
LOCUS	AF490511	2826 bp mRNA linear MAM 31-JUL-2002	
DEFINITION		Canis familiaris cyclic nucleotide gated channel beta subunit (CNGB3) mRNA, complete cds.	
ACCESSION	AF490511		
VERSION			
KEYWORDS	AF490511.1	GI:22023792	
SOURCE			
ORGANISM			
		Canis familiaris (dog)	
		Canis familiaris	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	
REFERENCE		1 (bases 1 to 2826)	
AUTHORS		Sidjanin,D.J., Lowe,J.K., McElwee,J.L., Milne,B.S., Phippen,T.M., Sargan,D.R., Aguirre,G.D., Acland,G.M. and Ostrander,E.A.	
TITLE		Canine CNGB3 mutations establish cone degeneration as orthologous to the human achromatopsia locus ACHM3	
JOURNAL		Hum. Mol. Genet. 11 (16), 1823-1833 (2002)	
PUBMED		12140185	
REFERENCES		2 (bases 1 to 2826)	
AUTHORS		Sidjanin,D.J., Lowe,J.K., McElwee,J.L., Milne,B.S., Phippen,T.M., Sargan,D.R., Aguirre,G.D., Acland,G.M. and Ostrander,E.A.	
TITLE		Direct Submission	
JOURNAL		Submitted (05-MAR-2002) Baker Institute, Cornell University, Hungerford Hill Rd., Ithaca, NY 14853, USA	
FEATURES			
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gene			
CDS			

## QSIRRAALPROTTROSLLIISMAPSABAGEEVLITIEVKEKAKQ"

## ORIGIN

Query Match 69.2%; Score 1682.2; DB 4; Length 2826;  
Beat Local Similarity 83.6%; Pred. No. 3.9e-313;  
Matches 1972; Conservative 0; Mismatches 312; Indels 75; Gaps 3;

Qy 78 GAATGAAGAGGCTCTCCACCAAGTAATCAGTCTCAGCAAAACCAGACAGGAGAGAAA 137  
Db 84 GAATGAAGAGGCTCTCCACCAAGTAATCAGTCTCAGCAAAACCAGACAGGAGAGAAA 143  
Qy 138 CAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAATCCAGTCAAGTCTGAAGAGCCACA 197  
Db 144 CAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAATCCAGTCAAGTCTGAAGAGCCACA 203  
Qy 198 CACCAACATCAAGACAAACTCTCCAGAAATAATCTCGAGATCTGACCAACAAACC 257  
Db 204 TGCCAAATGCAAGATAAATCTCGAGATAAATCTCAAGACCTGACGACAAATCC 263  
Qy 258 TGACCCCTCAAAATGACAGAACCAACTGGAAACAGTGCAGAGCAGAGAGAAATGGACCC 317  
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Qy 318 CGGGAAGAGGTCGAAACAGCCGCAAAACAAACCGGCTGAGCTCTGTTATAATGA 377  
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Qy 438 CAAGAAAGTGGTAGAGGAGATCTCTCTCAACCGAAGCCAGCCACAACTGCAAA 497  
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Qy 498 GCCACGGCTGTACACAGTAAAGAAAGCGATGATAAGCCAA---CAGAACTACTA 554  
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Qy 555 CAGGCTGTGGTTCAGAGTCAAAAGATGCTTTTACAGAGTACTTAAAGCGAATTA 614  
Db 564 TCACATATGTGTTTTAAATTCAGAGATGCTCTGACAGAGTACCTTAAAGCGAATTA 623  
Qy 615 ACTTCCAAACAGCATAGATTCATACAGATCGACTCTATCTCTGTGGCTCTTGTCTGT 674  
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Qy 735 AACCGCAGACATACACTACTGCTTATTCGGACATCATATGTGATCATCTACCT 794  
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Qy 795 TTATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTGAAGAGGAGACATAATAGT 854  
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Db 924 GTCAGTAAATGCTTTGATGTTTTTACCTCTCTTTGGGTTAATCCAGTATTTAGGAT 983  
Qy 975 AAATAGGATGTTAAAGTACACTTCATTTTTTGAATTTAATCATCACCTAGAGTCTATAAT 1034  
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Db 1824 TGCCAAATGATAGCCCATGGTTTTGCAATCTTTTAACTCTGCAAAAAGACCTCTCA 1883  
Qy 1875 AGAAATTTCTAGTCATTTATCCAGATTTCTGAAGGATCTCTATGAAGAGCCAGAGTCT 1934  
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Qy 1935 TTTAAAGCAGAGCTTAAGACCGCAGAGCAACCCCTCCAAAGAAAGATCTTTGGCTCTCT 1994  
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Qy 1995 CTTCCCAACCAAGAGAGACACCAACTGTTTTAAACTCTCTAGGAGCCACAGGAA 2054  
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Qy 2172 AGATAAACAAGAAAGAAATGAAGATAAAGGAAAAAGAAATCAAGATAAAGCAAGGAAG 2231  
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Db 2355 AGAAAGGCTAAGCAATAA 2373

RESULT 4  
LOCUS MMU243572  
DEFINITION Mus musculus mRNA for cyclic nucleotide-gated channel subunit CN66  
ACCESSION AJ243572  
VERSION AJ243572.1 GI:6851039  
KEYWORDS CN66 gene; cyclic nucleotide-gated channel; subunit CN66.  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 Gerstner,A., Zong,X., Hofmann,F. and Biel,M.  
AUTHORS Molecular cloning and functional characterization of a new  
TITLE modulatory cyclic nucleotide-gated channel subunit from mouse  
JOURNAL J. Neurosci. 20 (4), 1324-1332 (2000)  
MEDLINE 20130348  
PubMed 10662822  
REFERENCE 2 (bases 1 to 4710)  
AUTHORS Gerstner,A.  
TITLE Direct Submission  
JOURNAL Submitted (26-JUL-1999) Gerstner A., Technische Universitaet Muenchen, Pharmakologie und Toxikologie, Biedersteiner Str. 29, D-80802 Muenchen, GERMANY

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ORIGIN

Query Match 56.1%; Score 1362.4; DB 10; Length 4710;  
Best Local Similarity 76.2%; Pred. No. 8.9e-252;  
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy 1515 GGTCCAGTTAGCCCTCGCCATTTGATGTGAATCTCAGCATCATCAAGAAATGCTAGTTT 1574
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy 2235 GCCAAGAGAGAGCCACTGGACAGACCTGAATGTACAGCAAGTCTCTATTGAGTGGAGGA 2294
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 5
LOCUS CQ716885 1350 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 2819 from Patent WO02068579.
ACCESSION CQ716885
VERSION CQ716885.1 GI:42277742
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 2819 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source
location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 35.1%; Score 853.4; DB 6; Length 1350;
Best Local Similarity 99.9%; Pred. No. 7.1e-154;
Matches 854; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 ATGTTTAAATCGCTGACAAAAGTCAACAAGTGAAGCTTATAGGAGAGAAATGAGNAT 60
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Qy 121 ACAGCACAGGAGAAAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTC 180
Db 121 ACAGCACAGGAGAAAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTC 180
Qy 181 ACGTCTGAAGGCCACACACCAACATACAGACAAACTCTCCAAGAAAAAATTCCTCTGGA 240
Db 181 ACGTCTGAAGGCCACACACCAACATACAGACAAACTCTCCAAGAAAAAATTCCTCTGGA 240
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QY	241	GATCTGACCAACAACCCCTGACCTCAAAATGACAGAGAACCAACTGGAAACAGTGCACAG	300
Db	241	GATCTGACCAACAACCCCTGACCTCAAAATGACAGAGAACCAACTGGAAACAGTGCACAG	300
QY	301	CAGAAGGAATGGACCCCGGGAAGAAGGTCCAAACAGGCCACAAAACAAACCCCTGCA	360
Db	301	CAGAAGGAATGGACCCCGGGAAGAAGGTCCAAACAGGCCACAAAACAAACCCCTGCA	360
QY	361	GCTCTGTTATAATAGTATGCCGATGCCAGTCCAGCTACACACCTGGTGAAGAAGTCCGT	420
Db	361	GCTCTGTTATAATAGTATGCCGATGCCAGTCCAGCTACACACCTGGTGAAGAAGTCCGT	420
QY	421	CAAGAAGACAGCCCTCTACAAGAAAAAGTTGGTAGAGGAGATCTCTCTCACCCGAAGCC	480
Db	421	CAAGAAGACAGCCCTCTACAAGAAAAAGTTGGTAGAGGAGATCTCTCTCACCCGAAGCC	480
QY	481	AGCCCAAACTGCAAGGCCACCGCTGTACCAAGTAAAGAAAGCGATGATAAGCCA	540
Db	481	AGCCCAAACTGCAAGGCCACCGCTGTACCAAGTAAAGAAAGCGATGATAAGCCA	540
QY	541	ACAGAACTACTACAGCTGTCTGTGTTCAAAAGTCAAAAGATGCCCTTTAAACAGATAC	600
Db	541	ACAGAACTACTACAGCTGTCTGTGTTCAAAAGTCAAAAGATGCCCTTTAAACAGATAC	600
QY	601	TAAAGCGAATTAACCTTCAAAACAGCATAGATTATACACAGATCGACTCTATCTCCTG	660
Db	601	TAAAGCGAATTAACCTTCAAAACAGCATAGATTATACACAGATCGACTCTATCTCCTG	660
QY	661	TGGCTCTGCTGTGCTCTTGGCTTAACTGGAACCTGCTGGTTTATACACCTCGCGCTC	720
Db	661	TGGCTCTGCTGTGCTCTTGGCTTAACTGGAACCTGCTGGTTTATACACCTCGCGCTC	720
QY	721	GTCTTCCCATCAAAACCGCAGACAACATACCTACTGCGCTTATGCGGACATCATATGT	780
Db	721	GTCTTCCCATCAAAACCGCAGACAACATACCTACTGCGCTTATGCGGACATCATATGT	780
QY	781	GATATCATCTACCTTTATGATATGCTATTTATCCAGCCACAGACTCCAGTTTGTAAAGAG	840
Db	781	GATATCATCTACCTTTATGATATGCTATTTATCCAGCCACAGACTCCAGTTTGTAAAGAG	840
QY	841	GGAGACATAATAGTG 855	
Db	841	GGAGACATAATAGTG 855	
RESULT 6			
HUMNGCCB			
LOCUS			
DEFINITION			
Homo sapiens clone hRNC2a retinal rod cyclic nucleotide-gated cation channel gene, complete cds.			
L15297			
ACCESSION			
L15297.1 GI:291914			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
Chen,T.Y., Peng,Y.W., Dhallan,R.S., Ahamed,B., Reed,R.R. and Yau,K.W.			
REFERENCE			
AUTHORS			
A new subunit of the cyclic nucleotide-gated cation channel in retinal rods			
Nature 362 (6422), 764-767 (1993)			
JOURNAL			
MEDLINE			
PUBMED			
93226050			
7682292			
REFERENCE			
2 (bases 1 to 3025)			
Ahamed,B.			
AUTHORS			
TITLE			
Direct Submission			
Submitted (17-MAY-1993) Basheer Ahamed, Biomedical Engineering, Johns Hopkins School of Medicine, Baltimore, MD 21205, USA			
JOURNAL			
COMMENT			
Original source text: Homo sapiens DNA.			
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Location/Qualifiers			

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		/tissue_type="retinal"	
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ORIGIN		Query Match	
		Best Local Similarity 23.8%; Score 577.4; DB 9; Length 3025;	
		Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;	
QY	617	TTCCAAAACAGATAGATTATACACAGATCGACTCTATCTCTCTGTGGCTCTTGTGTC	676
Db	635	TTCCCCAGAGCATTTGACCCGCTGACCACTGATGTATGTCTCTATGGCTGTCTTCTG	694
QY	677	CTCTTGCCTTATACTGGAACTGCTGCTTTATACCACTGCGCTCGCTCTTCCCATCAA	736
Db	695	TGATGCCCTGGAAATGGAACTGTGGCTGATTTCCGCTGCGCTTCCCTACCAGA	754
QY	737	CCGCGACACAATACACTACTGGCTTATTTGCGGACATCATATGTGATATCATCTACT	796
Db	755	CCCCGACAAATCATCCACCTGCTGCTGATGATTAACCTATGCGACCTCATCTACTTC	814
QY	797	ATGATATGCTATTTATCCAGCCCACTCCAGTTTGTAAAGAGGAGAGACATAAATAG	856
Db	815	TGGACATCACCGTGTTCAGACACACGCTCGACTTTGTTCAGAGCGCGGACATCATTC	874
QY	857	ATTCAAAATGAGCTAAGGAAACACTACAGACTTCTACAAAATTTTCAGTTGGATGCG	916
Db	875	ACAAAAGACATGCGAAATAACTACTGAGTCTCGCGCTTCAAGATGGACCTGCTCA	934
QY	917	CAATAATACCAATTTGATATTTGCTACCTCTTTCTTTGGGTTTAATCCAATGTTAG	976
Db	935	GCCTCCTGCTTGGATTTTCTCTATTTGAAAGTCGGTGTGAACCCCTCTCCGCTGC	994
QY	977	ATAGATGTTAAAGTACACTTCATTTTGAATTTTAATCATCACCTAGAGTCTATAATG	1036
Db	995	CCCGCTGTTTAAAGTACATGGCTTCTTCGAGTTTAAACAGCGCGCTGGAATCCATC	1054
QY	1037	ACAAAAGCATATATCTACAGAGTTATTTCGAAACAACTGGATACTTGTCTTTATTCG	1096
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QY	1097	TTAATGCCCTGTTTATTACTGGGCTTCAAACTATGAAGGAATTTGGCACTACTAGATG	1156
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QY	1157	TGTATGATGGGAGGAAACGAGTATCTGAGATGTTATTATTGGGCACTTGAACCTTAA	1216
Db	1175	TTTACGATGGCGTGGGAAACAGTTATATTCGCTGTACTACTTGTGTGAAGACCTCA	1234
QY	1217	TTACCATTTGGTGGCTTCCGAAACCAACCTTTTATTGAAATTTGTTTCAACTCTTTGA	1276
Db	1235	TCACCATCGGGGGCTGCTGACCCCAAGACACTCTTTGAAATTTGCTTCCAGCTGCTGA	1294
QY	1277	ATTTTTTTCTGGAGTTTCTGTTCTCCAGTTTAAATTTGGTCAGATGAGATGTGATTG	1336





Db	1549	TTTACGATGGCGTGGGAAACAGTTATATTGCTGTTACTACTTTGCTGTGAGAACCTCTCA	1609
Qy	1217	TTACCATTTGGTGGCTTCCAGAACCAAACTTTATTTTGAAATTTGTTTTCAACTCTTGA	1276
Db	1609	TCACCATCGGGGGTGCTGACCCCAAGACACTCTTTGAAATTTGCTTCCAGCTGCTGA	1668
Qy	1277	ATTTTTTTTCTGAGAGTTTTTGGTTCCTCCAGTTTAAATTTGTCAGATCAGAGATGTGATTG	1336
Db	1669	ATTATTTTACGGGGCGTCTTTCCTTTCTCTGTGATGATCGGACAGATGAGAGATGTGGTAG	1728
Qy	1337	GAGCAGCTTACAGCCAAATCAGAACTACTTTCCGCGCTCGCATGGATGACACCAATTGCCTTACA	1396
Db	1729	GGGCGGCACCGCGGGACAGACCTTACTAGCGCAGCTCATGGACAGCACGCTGAAGTACA	1788
Qy	1397	TGAACAATTACTCCATTTCTTAACTTTGTGCNAAAGCAGTTTCGAGCTTGGTATGAATATA	1456
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Qy	1457	CATGGGACTCTCAAAGAAATGCTAGATCAGTCTGATTTTGTCTTAAGACCTTACCAACTACGG	1516
Db	1849	CCTGGCACTCGCAAGGATGCTGTGATGAGTCAGAGCTGATGGTGCAGCTTCCAGACAAGA	1908
Qy	1517	TCCAGTTAGCCCTCGCCATTGATGTGAACCTTCAGCATCATCAGCAAAAGTCGACTTGTTC	1576
Db	1909	TGCGGCTGGACCTCGCCCATCGACGTGAACTACAACTCGTTAGCAAAAGTCGCACTCTTTC	1968
Qy	1577	AGGGTGTGTATACACAGATGATTTATGACATGTTGCTTAAGATTGAAATCCGTTCTCTATT	1636
Db	1969	AGGGCTGTGACCGGCAGATGATCTTTGACATGCTGAAGAGGCTTCGCTCTGTTGTCTTACC	2028
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Db	2029	TGCCAACGACTATGTGTGCAAGAAGGGGAGATCGGCCGTGAGATGATCATCATCCAGG	2088
Qy	1697	ATGGAAGATCCAAATTCTTTGGAGGCCCTGATGTTACTTAAAGTTCTGGTTACTCTGAAG	1756
Db	2089	CAGGGCAAGTGCAGGTCTTGGCGGCCCTCATGCGGAAATCTGTCTGTGTGACGCTGAAAG	2148
Qy	1757	CTGGGTCGGTGTTTGGAGAAATCAGCCCTCTTAGCAGCAGGAGGAGAAACCGTCGAACTG	1816
Db	2149	CTGGATCTGTGTTGGAGAAATAAGCTTGCTGGCTGTGGGGCGGNAACCGGGCACGG	2208
Qy	1817	CCAAATGGTGGGCCACGGGTTTGCCAAATCTTTTAACTCTAGACAAAGAACCTCCAAAG	1876
Db	2209	CCAACTGGTGGGCCACGGGTTTACCAACCTCTTCATCTCTGGATTAAGAGAGCACTGAAATG	2268
Qy	1877	AAATTTCTAGTGCATTATCCAGATTTCTGAAAGGATCCATCAAGAAAGCCAGAGTGTCTT	1936
Db	2269	AGATTTTGGTGCATTATCTCTAGTCTCAGAAGTTACTTCGGAAGAAAGCCAGCGCATGC	2328
Qy	1937	TAAAGCAGAAGGCTTAAGACCGCAGAAG	1963
Db	2329	TGAGAAGCAACAATAAGCCCCAAGGAGG	2355
RESULT 8			
HSU58837			
LOCUS			
DEFINITION	HSU58837	4033 bp	mRNA linear PRI 18-JUL-1997
ACCESSION	U58837	Human cGMP-gated cation channel beta subunit (CNCG2)	mRNA, complete cds.
VERSION	U58837.1	GI:1518638	
KEYWORDS			
SOURCE			
ORGANISM			
			Homo sapiens (human)
REFERENCE			Homo sapiens
AUTHORS			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
TITLE			1 (bases 1 to 930)
			Ardell,M.D., Makhija,A.K., Oliveira,L., Miniou,P., Viegas-Pequignot,E. and Fittler,S.J.
			CNCG3L, a homolog of the third subunit of bovine photoreceptor cGMP-gated channel





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ORIGIN

Query Match	23.8%;	Score 577.4;	DB 9;	Length 4382;
Best Local Similarity	64.3%;	Pred. No. 6.9e-101;		
Matches 866;	Conservative 0;	Mismatches 481;	Indels 0;	Gaps 0;
QY	617	TTCCAAACAGCATAGATTATACACAGATCGACTCTATCTCTCTGTGGCTCTTCTTGTCA	676	
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QY	677	CTCTTGGCTATAACTGGAACCTGCTGTTTATACACATCGCGCCCTCGTCTTCCCATATCAA	736	
Db	2043	TGATGGCTGGAATTGGAACCTGTTGGCTGATTCCTCCGTGGCTTCCCTTACCGA	2102	
QY	737	CCCGACAGACATACACTACTGCTGTTATGCGGACATCATATCTGATATCATCTACTT	796	
Db	2103	CCCGGACACATCCACCACTGGCTGCTGATGATTAACCTATGCGACCTCATCTACTTC	2162	
QY	797	ATGATATGCTATTATTATCCAGCCAGACTCCAGTTCCTGTAAGAGAGAGACATAATAGTG	856	
Db	2163	TGGACATCACCGTGTCCAGACACGCTGCGAGTTTGTGAGAGCGGGACATCATACGG	2222	
QY	857	ATTCAAAATGAGCTAAGAAACACTACAGGACTTCTACAAATTTCAAGTTGGATGTCGAT	916	
Db	2223	ACAAAAGGACATCGCAATAAATACTACCTGAAGTCTCGCGCTTCAAGATGGACCTGCTCA	2282	
QY	917	CAATAATACATTTGATATTGCTACTCTTCTTGGGTTTAACTCAATGTTAGACAA	976	
Db	2283	GCCTCTCGCCCTTGGATTTTCTTATTGAAAGTCGGTGAACCCCTCTCCGCTGC	2342	
QY	977	ATAGGATGTTAAAGTACACTTCAATTTTGAATTAATCATCACTAGAGTCTATATGG	1036	
Db	2343	CCCGCTGTTTAAAGTACATGCGCTTCTCGAGTTTAAACGCCCTGGAATCACTCTCA	2402	
QY	1037	ACAAAGCATATATCTACAGAGTTATTTCGAACAACTGGATCTGCTGTTTATTCGACAA	1096	
Db	2403	GCAAGCCCTACGTGTACAGGCTCATCAGGACCAACAGCTACCTTCTCTACAGCCTGAT	2462	
QY	1097	TTAATCGCTGTTTATTACTGGCTTCAAACTATGAAGAAATGGCACTACTAGATGG	1156	
Db	2463	TGAATTCCTGCTTATTACTGGGCACTCGGCTTATCAGGCGCTCGGCTCACTACTGGG	2522	
QY	1157	TGTATGATGGGAAGAAACGAGTATCTGAGATGTTTATTATTGGGCGAGTTTCAACTTTAA	1216	
Db	2523	TTTACGATGGCGTGGGAACAGTTATATTCGCTGTTACTTCTGCTGTAAGACCCCTCA	2582	
QY	1217	TTACCAATGGTGGCTTCCAGAACCAACTTTATTGAAATGTTTTCCTTCACTCTTGA	1276	
Db	2583	TCACCATCGGGGCTCGCTGACCCCAAGACACTCTTTGAAATGTTCTTCCAGCTGCTCA	2642	
QY	1277	ATTTTTTCTGAGTTTGTGCTTCTCCAGTTTAACTGGTCAGATGAGATGTCATGG	1336	
Db	2643	ATTATTTCAGGGCGCTTGTGCTTCTCTGTGATGATCGACAGATGAGAGATGTTGGTAG	2702	
QY	1337	GAGCAGCTACAGCAATCAGAACTACTTCGCGCCTGCTGATGATGACACCATTTGCTTACA	1396	

Db	2703	GGSCGCCACC CGGGGACAGACCTACTACCGCAGCTGCATGGACACACGGTGAAGTACA	2762	
QY	1397	TGAACAATTAATCTCCATTCTTAACCTTGTGCAAAAGGAGTTCCGACTTGGTATGAATATA	1456	
Db	2763	TGAATTTCTACAAAGATCCCCAAGTCGGTCAGAAACCGCGTCAAGACTCGGTACGAGTACA	2822	
QY	1457	CATGGGACTCTCAAGAATGCTAGATGAGTCTGATTGCTTAAGACCCCTACCAACTACGG	1516	
Db	2823	CTTGGCACTTCGCAAGCATGCTGGATGAGTCAGACTGATGGTCAGCTTCCAGACAAGA	2882	
QY	1517	TCCAGTTAGCCCTCGCAATTGATGTGAACCTTCAGCATCATACGAAAGTCGACTTGTTC	1576	
Db	2883	TGCGGCTGACCTCGCATCGAGCTGAACATAACAATCGTTCGAAAGTCGCACTCTTTC	2942	
QY	1577	AGGTTGTGATACACAGATGATTATGACATGTTGCTAAGATGAAATCGGTTCTCTATT	1636	
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QY	1637	TGCTGTGCTGTTCTGCAAAAAGGAGAAATTTGGCAAGGAAATGTATATCATCAAGC	1696	
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QY	1697	ATGGAGAACTCCAAGTTCTTGAGGCGCTGATGGTACTTAAAGTTCTGTTACTCTGAAAG	1756	
Db	3063	CAGGGCAAGTGCAAGTCTTGGGCGGCTGATGGGAAATCTGTGCTGTGTGACGCTGAAAG	3122	
QY	1757	CTGGGTCGTTGTTGGAGAAATCAGCTTCTAGCAGCAGGAGGAGAAACCGTCGAACTG	1816	
Db	3123	CTGGATCTGTGTTGGAGAAATAAGCTTGTGCTGGCTGTTGGGGCGGGAACCGCGCACGG	3182	
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QY	1877	AAATTTCTAGTCAATTATCCAGATTCTGAAGGATCTCATGAAGAACCCAGAGTGCCTT	1936	
Db	3243	AGATTTTGTGCTATCTCTGAGTCTCAGAAGTTACTTCGGAAGAAAGCCAGCGCATGC	3302	
QY	1937	TAAAGCAGNAGGCTAAGACCGCAGAAAG	1963	
Db	3303	TGAGAAGCAACAATAAGCCCAAGGAGG	3329	

RESULT 10  
CQ715550  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
Kits, such as nucleic acid arrays, comprising a majority of  
humanexons or transcripts, for detecting expression and other uses  
thereof  
Patent: WO 02068579-A 1484 06-SEP-2002;  
PE Corporation (NV) (US)  
Location/Qualifiers  
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ORIGIN

Query Match 23.7%; Score 575.8; DB 6; Length 4320;  
Best Local Similarity 64.2%; Pred. No. 1.4e-100;  
Matches 865; Conservative 0; Mismatches 482; Indels 0; Gaps 0;

Qy	617	TTCCAAACAGC	ATAGATT	CATACAGAT	TCGACT	TA	CTCCTCGTGGCTCTT	GTGTGCA	676
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Qy	677	CTCTTGGCCT	ATAACTGGAACT	GTGGTTT	ATACCACT	GGCGCTCGT	CTTCCCATATCAAA	736	
Db	1988	TGATGGCCT	TGGAAATTGG	AACTTGG	CTGATACCT	TATGGACCTCAT	CTACTTCTTC	2047	
Qy	737	CCGAGACAAC	ATACATCTAC	TCTGGCTT	ATTGCGGAC	ATCATATGT	GTGATATCATCTACCTTT	796	
Db	2048	CCCGGACAA	CATCCACCACT	GGCTGCTG	TATACCTAT	TGGACCTCAT	CTACTTCTTC	2107	
Qy	797	ATGATATGCT	ATTTATCAG	CCCCAGACT	CTCAGATTT	TGTAAGAGGAGGAG	AGACATATATG	856	
Db	2108	TGSGACAT	CACCGTGTTC	CAGACACG	CCCTGCAGTTT	TGTCAGAGGCGGGAG	CATCATTTACGG	2167	
Qy	857	ATTCAAAT	TGACTAAGGAA	ACATACAGG	ACTCTACAAAAT	TTTCAGTTCCGAT	TCGCAT	916	
Db	2168	ACAAAAGG	CATCGGAAT	AACTACCTG	AAAGTCTCGCCGCTT	CAAGATG	GAACCTGTCA	2227	
Qy	917	CAATAATAC	CAATTTGTAT	TTGTACCTCT	TTCTTTGGTGT	TAATCCAAT	GTTTAGAGCAA	976	
Db	2228	GCCTCTGCC	CTTGAATTTCT	CTATTGAA	AGTCGGTGTGA	ACCCCTCTCG	CGCTGC	2287	
Qy	977	ATAGATGTT	AAAGTACACT	TCATTTTTT	TGAATTAAT	ATCATCACT	AGATCTATATAG	1036	
Db	2288	CCCCTGTTT	AAAGTACATG	CGCTTCTTCGAGTT	TTAACAGCG	CGCTGGAATCCAT	CTCATCTCA	2347	
Qy	1037	ACAAAGCAT	ATATCTACAG	AGTTATTCGA	CACTGTGAT	ACTTGTCTGTT	TTATTTCTGCACA	1096	
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Db	2408	TGAATTCCT	GTCTTTATCTG	GGCATCG	GCCTATCAGGG	CGCTCGCTCCAC	CTCATCTGGG	2467	
Qy	1157	TGTATGAT	GGGGAAGG	AAACGAGT	ATCTGAGAT	GTGTTATTATGG	CGAGTTTCGAACTTTAA	1216	
Db	2468	TTTACGAT	TGGCGTGGG	AAACAGTTAT	TCGCTGTACT	TTTGTCTG	TGTAAGACCTCA	2527	
Qy	1217	TTACCAT	TGGTGGCTTCC	AGAACCAAA	ACTTTATTTGAA	ATTTGTTTTTCAA	CTCTTGA	1276	
Db	2528	TCACCAT	TGGGGGCTCG	CTGACCC	CAAGACACTCTTT	TGAAATTTGCTTCC	AGCTGTGA	2587	
Qy	1277	ATTTTTTT	CTGAGTTTTGT	GTCTTCCAG	TTTTAATTTG	TCAGATGAGAG	ATGTCATTCG	1336	
Db	2588	ATTAATTT	CACGGGCTCTT	GTCTTCTGT	GATGATCGG	ACAGATGAG	AGATGTGGTAG	2647	
Qy	1337	GAGCAGCT	CAGCCAAATC	AGAACTACTT	CCGCGCTG	CATGATGAC	CAACATTTGCC	1396	
Db	2648	GGGCGCCA	CCGCGAGGAC	AGACCTACTAC	CCGAGCTG	CATGGACAG	CACGGTGAAGTACA	2707	
Qy	1397	TGAACAAT	TACTCAATTC	CTTAACCTTG	TGCAAAAGCG	AGTTCCGAC	CTTGGATGGAATATA	1456	
Db	2708	TGAATTTT	CTCAAGATCCC	AGGTCCGTG	CAGAAACCG	CGTCAAGAC	CTGTGTAGAGTACA	2767	
Qy	1457	CATGGGACT	CTCAAAGATG	CTAGATCAG	TCTGATTTG	CTTTAGACCC	TACCACTACCG	1516	
Db	2768	CCTGGCACT	CGCAAGGCAT	GCTGGATG	ATGTCAGAG	CTGATGGT	GCAGCTTCCAGACAA	2827	
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Qy	1577	AGGTTGTG	ATACAGATG	ATTAAGCA	TGTTGTGTA	AGATTTGAA	ATCGGTTCTCTAT	1636	
Db	2888	AGGGCTG	TGACCGG	CAGATGATCTT	TGACATGCTG	AAAGGGCTTCG	CTCTGTGTCTACC	2947	
Qy	1637	TGCTGTGT	ACTTTGTCTG	CAAAAGGG	AGAAATGG	CAAGGAAATG	TATATCATCAAG	1696	
Db	2948	TGCCCAAC	GACTATGTGT	CAAGAGGG	GAGATCGG	CGTGAGTATG	TATCATCATCCAG	3007	
Qy	1697	ATGAGAAG	TCCAAGTTCT	TTTGGAGG	CCCTGATGGT	ACTAAAGTTCT	GTGTTACTCTCAAG	1756	

Db	3008	CAGGCGAAGTGCAGGTCTTGGCGGCCCTGATGGAAATCTGTCTGGTCACGCTGAAG	3067
Qy	1757	CTGGTCCGGTGTTTGGAGAAATCAGCCCTTCTAGCAGCAGGAGGAGAAACCGTCGAATG	1816
Db	3068	CTGGATCTGTGTTTGGAGAAATAAGCTTGTGGCTGTGGGGCGGGAACCGGCGCACGG	3127
Qy	1817	CCAATGTGGTGGCCCGCACGGTTCGCCAATCTTTTAATCTAGACAAAGACCCCTCCAAG	1876
Db	3128	CCACGTGTGGCGCACGGTTTACCAACTCTTCATCTCGATAGAGGACCTGAATG	3187
Qy	1877	AAATTCATGTGCATTATCCAGATTCTGAAAGGATCCTCATGAGAAAGCCAGAGTGCCTT	1936
Db	3188	AGATTTTGGTGCATTATCTCCGTAGTCTCAGAAGTTACTCCGGAAGAAAGCCAGGCGCATG	3247
Qy	1937	TAAAGCAGAAGGCTTAAGACCCGCAAG	1963
Db	3248	TGAGAAGCAACAATAAGCCCCAAGSAGG	3274

RESULT 11	BC045114	4763 bp	mrna	linear	ROD 03-AUG-2004
LOCUS	BC045114				
DEFINITION	Mus musculus cyclic nucleotide gated channel beta 1b, mRNA (CDNA clone IMAGE:450435), partial cds.				
ACCESSION	BC045114				
VERSION	1	GI:28175674			
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 4763)				
AUTHORS	Srausberg, R.L., Reingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zebberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ussidi, T.B., Toshlyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S.S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smallos, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 4763)				
AUTHORS	Director MGC Project.				
TITLE	Direct Submission				
JOURNAL	Submitted (27-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>				
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgabs-r@mail.nih.gov">cgabs-r@mail.nih.gov</a> Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a> Contact: <a href="mailto:nisc_mgc@hri.nih.gov">nisc_mgc@hri.nih.gov</a>				





QY 1757 CTGGTCGGTGTGTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGAGAAACCGTCGAACCTG 1816  
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RESULT 13  
AF074013  
LOCUS Bos taurus cyclic nucleotide-gated channel beta subunit 1d  
DEFINITION (CNCbeta) mRNA, complete cds.  
ACCESSION AF074013  
VERSION AF074013.1 GI:3309623  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 3090)  
Wiesner,B., Weiner,J., Middendorff,R., Hagen,V., Kaupp,U.B. and  
Weyand,I.  
Cyclic nucleotide-gated channels on the flagellum control Ca2+  
entry into sperm  
J. Cell Biol. 142 (2), 473-484 (1998)  
98345361  
PUBMED 9679145  
REFERENCE 2 (bases 1 to 3090)  
Wiesner,B., Weiner,J., Middendorff,R., Hagen,V., Kaupp,U.B. and  
Weyand,I.  
TITLE Direct Submission  
Submitted (24-JUN-1998) FBI, FZ-Juelich, Leo-Brandt-Strasse,  
Juelich, NRW 52425, Germany  
Location/Qualifiers  
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ORIGIN  
Query Match 23.5%; Score 572.2; DB 4; Length 3090;  
Best Local Similarity 64.1%; Pred. No. 7.2e-100;  
Matches 862; Conservative 0; Mismatches 483; Indels 0; Gaps 0;  
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RESULT 14  
BTNG4CGN  
LOCUS BTNG4CGN 3253 bp mRNA linear MAM 16-APR-1996  
DEFINITION B.taurus mRNA for CNG4c protein.  
ACCESSION X94707  
VERSION X94707.1 GI:1154636  
KEYWORDS CNG4c gene; CNG4c protein; cyclic nucleotide-gated cation channel; modulatory subunit.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
1  
Biel, M., Zong, X., Ludwig, A., Sauter, A. and Hofmann, F.  
Molecular cloning and expression of the Modulatory subunit of the cyclic nucleotide-gated cation channel  
J. Biol. Chem. 271 (11), 6349-6355 (1996)  
96198098  
8626431  
2 (bases 1 to 3253)  
Biel, M.  
Direct Submission  
Submitted (08-JAN-1996) M. Biel, Inst. f. Pharmakologie und Toxikologie, Technische Universitaet Muenchen, 80802 Muenchen, Biedersteiner Strasse 29, FRG  
Location/Qualifiers  
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(CNCbeta) mRNA, complete cds.  
ACCESSION AF074014  
VERSION AF074014.1  
KEYWORDS GI:3309625  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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1 (bases 1 to 3290)  
Wiesner,B., Weiner,J., Middendorff,R., Hagen,V., Kaupp,U.B. and  
Weyand,I.  
TITLE Cyclic nucleotide-gated channels on the flagellum control Ca2+  
entry into sperm  
J. Cell Biol. 142 (2), 473-484 (1998)  
MEDLINE 98345361  
PUBMED 9679145

REFERENCE 2 (bases 1 to 3290)  
Wiesner,B., Weiner,J., Middendorff,R., Hagen,V., Kaupp,U.B. and  
Weyand,I.  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

Weyand,I.  
Direct Submission  
Submitted (24-JUN-1998) IBI, FZ-Juelich, Leo-Brandt-Strasse,  
Juelich, NRW 52425, Germany  
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ORIGIN

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Search completed: March 27, 2005, 16:03:45  
Job time : 10112 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 27, 2005, 03:41:23 ; Search time 1203 Seconds  
(without alignments)  
11957.582 Million cell updates/sec

Title: US-09-855-828-3  
Perfect score: 2430  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004as:\*

13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2430	100.0	2757	6	AAD25729 Human cyc
2	654.4	26.9	2516	5	AAS69653 DNA encod
3	579	23.8	4380	13	ACN42631 Human dia
4	577.4	23.8	2607	8	ABZ80565 Nucleotid
5	573.6	23.6	3811	5	AAS91658 DNA encod
6	569.6	23.4	4238	10	ADB53355 Primary r
7	568	23.4	3236	13	ADS64556 Norway ra
8	518	21.3	2244	5	AAS76156 DNA encod
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10	223	9.2	3275	4	ABL19457 Drosophil
11	176.4	7.3	2500	10	ADD93243 Cyclic nu
12	176.4	7.3	2500	13	ADR24566 Breast ca
13	160.6	6.6	289	5	AAS75291 DNA encod
14	136.2	5.6	2109	4	ABL18085 Drosophil
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22	129	5.3	526	4	ABA61898	AbA61898 Human foe
23	129	5.3	526	4	AAI41823	Aai41823 Probe #10
24	129	5.3	526	4	Aak36108	Aak36108 Human bon
25	129	5.3	526	4	AAK10209	Aak10209 Human bra
26	129	5.3	526	4	ABS35801	AbS35801 Human liv
27	128.4	5.3	1995	8	AAD56242	Aad56242 Rat CNG c
28	128.4	5.3	1995	8	AAD56240	Aad56240 Rat CNG c
29	128	5.3	2877	10	ADF56507	Adf56507 Modified
30	127	5.2	127	4	ABA74393	AbA74393 Human foe
31	127	5.2	127	4	AAI54858	Aai54858 Probe #23
32	127	5.2	127	4	AAK49030	Aak49030 Human bon
33	127	5.2	127	4	AAK22857	Aak22857 Human bra
34	127	5.2	127	4	ABS48687	AbS48687 Human liv
35	124.4	5.1	5133	4	ABL14931	AbL14931 Drosophil
36	120.6	5.0	5692	4	ABL19456	AbL19456 Drosophil
37	116.8	4.8	1989	8	ABX94804	AbX94804 Bovine CN
38	116.8	4.8	3166	13	ADS64555	AdS64555 Bovine cy
39	115.2	4.7	1989	8	ABX94805	AbX94805 Bovine CN
40	115.2	4.7	1992	13	ADS64558	AdS64558 Cyclic nu
41	113.6	4.7	1989	8	ABX94806	AbX94806 Bovine tra
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44	111.2	4.6	1995	8	ABS58301	AbS58301 cDNA enco
45	111.2	4.6	1995	8	ABZ80563	AbZ80563 Nucleotid

ALIGNMENTS

RESULT 1.

AAD25729

ID AAD25729 standard; DNA; 2757 BP.

XX

AC AAD25729;

XX

DT 26-MAR-2002 (first entry)

XX

DE Human cyclic nucleotide-gated cation channel 3 beta subunit DNA.

XX

KW Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;

KW cyclic nucleotide-gated ion channel; contraceptive; vision disorder;

KW male infertility; genetic defect; reporter-ligand interaction; CNG;

KW viral infection; cancer; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

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FT FT /\*tag= a

FT FT /note= "These bases are absent in the sequence shown as

FT FT SEQ ID NO:2 in Page 64-65 of the specification"

FT CDS 112..2541

FT FT /\*tag= b

FT FT /product= "Human CNG3B protein"

FT FT /note= "This region is specifically claimed in claim 4 as

FT FT SEQ ID NO:4"

FT FT 2753..2757

FT FT /\*tag= c

FT FT /note= "These bases are absent in the sequence shown as

FT FT SEQ ID NO:2 in Page 64-65 of the specification"

PN WO200188090-A2.

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PD 22-NOV-2001.

XX

XX 15-MAY-2001; 2001WO-US015814.

PF

XX 15-MAY-2000; 2000US-0204445P.

PR

XX 14-MAY-2001; 2001US-00855828.

PA (ICAG-) ICAGEN INC.

XX

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DR	WPI: 2002-089847/12.	Qy	601	TTAAAGCGAATTAAACTTCCAAACACAGATAGATTTCATACACAGATCGACTCTATCTCCTG	660
DR	P-PSDB; RAE15982.	Db	712	TTAAAGCGAATTAAACTTCCAAACACAGATAGATTTCATACACAGATCGACTCTATCTCCTG	771
XX					
PT	New polypeptide, useful for screening for modulators of cyclic nucleotide	Qy	661	TGCTCTTGCTTGCTCACTCTTGCTCTATACTTGAACTGCTGGTTTATACCACTCGCGCTC	720
PT	-gated ion channels, comprises the isolated cyclic nucleotide-gated				
PT	cation channel 3 beta subunit.	Db	772	TGCTCTTGCTTGCTCACTCTTGCTCTATACTTGAACTGCTGGTTTATACCACTCGCGCTC	831
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PS	Claim 4; Fig 2; 83pp; English.	Qy	721	GTCTTCCCATATCAAAACCGACAGACAAATACACTACTGCTTATTTGCGGACATCATATGT	780
CC	The invention relates to human cyclic nucleotide-gated cation channel 3	Db	832	GTCTTCCCATATCAAAACCGACAGACAAATACACTACTGCTTATTTGCGGACATCATATGT	891
CC	beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member	Qy	781	GATATCATCTACCTTTATCATATGCTTATTTATCCAGCCAGACTCCAGTTTGTAAAGGA	840
CC	of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms	Db	892	GATATCATCTACCTTTATCATATGCTTATTTATCCAGCCAGACTCCAGTTTGTAAAGGA	951
CC	functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha	Qy	841	GGAGACATATAGTGGATTCAATGAGCTTAAGAAACACTACAGGACTTCTACAAAATTT	900
CC	subunits that are expressed in retina. CNG3B polypeptides are useful for	Db	952	GGAGACATATAGTGGATTCAATGAGCTTAAGAAACACTACAGGACTTCTACAAAATTT	1011
CC	screening modulators of CNGs which are useful as contraceptives and for	Qy	901	CAGTTGGATGTCCGATCAATATACATTTGATATTTGCTACTCTCTTTGGTTTAAAT	960
CC	treating various disorders involving cation channels, e.g. vision	Db	1012	CAGTTGGATGTCCGATCAATATACATTTGATATTTGCTACTCTCTTTGGTTTAAAT	1071
CC	disorders and male infertility. Polynucleotides of the invention are	Qy	961	CCANTGTTTAGAGCAATAGGATGTTAAAGTACACTTCAATTTTGAATTTTAAATCATAC	1020
CC	useful for transfection of cells in vitro and in vivo, to correct	Db	1072	CCANTGTTTAGAGCAATAGGATGTTAAAGTACACTTCAATTTTGAATTTTAAATCATAC	1131
CC	acquired and inherited genetic defects, cancer and viral infections.	Qy	1021	CTAGAGTCTATAATGGACAAAGCATATATCTACAGAGTTATTTGCAACAACTCGATCTTG	1080
CC	Sequences of the invention are useful as reporter molecules in assays and	Db	1132	CTAGAGTCTATAATGGACAAAGCATATATCTACAGAGTTATTTGCAACAACTCGATCTTG	1191
CC	detection systems, to measure changes in cation concentration, membrane	Qy	1081	CTGTTTATTTCTGCAATTAATCCCTGTGTTTATTAATCTGGGCTTCAAACTATGAAGAAAT	1140
CC	potential, current flow, ion flux, transcription, signal transduction,	Db	1192	CTGTTTATTTCTGCAATTAATCCCTGTGTTTATTAATCTGGGCTTCAAACTATGAAGAAAT	1251
CC	reporter-ligand interactions and second messenger concentrations, in	Qy	1141	GGCACTACTAGATGGTGTATGATGGGGAAGAAAGAGATATCTGAGATGTTTATTTATG	1200
CC	vitro, in vivo and ex vivo. They are useful to construct models of CNGs	Db	1252	GGCACTACTAGATGGTGTATGATGGGGAAGAAAGAGATATCTGAGATGTTTATTTATG	1311
CC	in a computer system and for examining expression and regulation of	Qy	1201	GCAGTTTCGAACTTTAAATTAACCAATGCTGGCTTTCAGAACCAACAACTTTATTTGAAAT	1260
CC	cation channels. The present sequence is a DNA encoding CNG3B protein	Db	1312	GCAGTTTCGAACTTTAAATTAACCAATGCTGGCTTTCAGAACCAACAACTTTATTTGAAAT	1371
XX					
SQ	Sequence 2757 BP; 946 A; 571 C; 581 G; 659 T; 0 U; 0 Other;	Qy	1261	GTCTTTCAACTCTTGAAATTTTCTGGAGTTTCTGAGTTTCTCCAGTTTAAATGGTCTAG	1320
	Query Match 100.0%; Score 2430; DB 6; Length 2757;	Db	1372	GTCTTTCAACTCTTGAAATTTTCTGGAGTTTCTGAGTTTCTCCAGTTTAAATGGTCTAG	1431
	Best Local Similarity 100.0%; Pred. No. 0;	Qy	1321	ATGAGAGATGTGATTTGGAGCAGCTACGCCAATCAGAACTACTCCGCGCTCGATGGAT	1380
	Matches 2430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	1432	ATGAGAGATGTGATTTGGAGCAGCTACGCCAATCAGAACTACTCCGCGCTCGATGGAT	1491
Qy	1 ATGTTTAAATCGTGCACAAAGTCAACAAGTGAAGCTTATAGGAGAGAACATGAGAAT	Qy	1381	GACACCATTTGCCCTACATGAAACAAATTAATCTCAATTCCTTAACTTGTGCAAAAGCGAGTTCGG	1440
Db	112 ATGTTTAAATCGTGCACAAAGTCAACAAGTGAAGCTTATAGGAGAGAACATGAGAAT	Db	1492	GACACCATTTGCCCTACATGAAACAAATTAATCTCAATTCCTTAACTTGTGCAAAAGCGAGTTCGG	1551
Qy	61 GAACAAGTTTCTGTCGGATGAGAGGCTCTCACCAGTAATCAGTCTCAGCAACC	Qy	1441	ACTTGGTATGAATATACATGGGACTCTCAAGAAGATGCTAGATGAGTCTGATTTGCTTAAG	1500
Db	172 GAACAAGTTTCTGTCGGATGAGAGGCTCTCACCAGTAATCAGTCTCAGCAACC	Db	1552	ACTTGGTATGAATATACATGGGACTCTCAAGAAGATGCTAGATGAGTCTGATTTGCTTAAG	1611
Qy	121 ACAGCAGGAGAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAATCCAGTC	Qy	1501	ACCTTACCNACTACCGGTCAGTTAGCCCTCGCACTTGTGAACTTCCAGCATCATCAGC	1560
Db	232 ACAGCAGGAGAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAATCCAGTC	Db	1612	ACCTTACCNACTACCGGTCAGTTAGCCCTCGCACTTGTGAACTTCCAGCATCATCAGC	1671
Qy	181 ACGTCTGAAGAGCCACACACCAACATACAGAACTCTCCAGAAATAATTCCTCTGGA	Qy	1561	AAAGTCGACTTGTTCAGAGGTTTGTGATACACAGATGATTTATGACATGTTGCTAAAGATTG	1620
Db	292 ACGTCTGAAGAGCCACACACCAACATACAGAACTCTCCAGAAATAATTCCTCTGGA	Db	1672	AAAGTCGACTTGTTCAGAGGTTTGTGATACACAGATGATTTATGACATGTTGCTAAAGATTG	1731
Qy	241 GATCTGACCAACACCTGACCTCAAAATGACGAGCAACCACTCGAACAGTGCAGAG	Qy	1621	AAATCCGTTCTCTATTTGCTGGTGAATTTGTCTGCAAAAAGGGAGAAATTTGGCAAGGAA	1680
Db	352 GATCTGACCAACACCTGACCTCAAAATGACGAGCAACCACTCGAACAGTGCAGAG	Db	1732	AAATCCGTTCTCTATTTGCTGGTGAATTTGTCTGCAAAAAGGGAGAAATTTGGCAAGGAA	1791
Qy	301 CAGAAGAAATGGACCCCGGGAAGAGGTCCAAACAGCCACCAAAACCGCTCGCA				
Db	412 CAGAAGAAATGGACCCCGGGAAGAGGTCCAAACAGCCACCAAAACCGCTCGCA				
Qy	361 GCTCTCTTTAATAGTATGCGATGCGGATGCGGCTACACAACTGCTGGTGAAGAATGCGT				
Db	472 GCTCTCTTTAATAGTATGCGATGCGGATGCGGCTACACAACTGCTGGTGAAGAATGCGT				
Qy	421 CAAAGAACAGCCCTCTACAGAAAGATTTGGTAGGGAGATCTCTCCCTCACCCGAGCC				
Db	532 CAAAGAACAGCCCTCTACAGAAAGATTTGGTAGGGAGATCTCTCCCTCACCCGAGCC				
Qy	481 AGCCCAAACTCAAGCCCGCTGTACACACAGTAAAGAAAGCGATGATAGGCA				
Db	592 AGCCCAAACTCAAGCCCGCTGTACACACAGTAAAGAAAGCGATGATAGGCA				
Qy	541 ACAGAACTTACTACAGGCTGTTGTTGTTCAAAAGTCAAAAGATGCTTTTAAACAGAGTAC				

Qy 1681 ATGTATATCATCAAGCATGGAGAGTCCAAAGTCTTTGGAGGCCCTGATGGTACTAAAGTT 1740  
Db 1792 ATGTATATCATCAAGCATGGAGAGTCCAAAGTCTTTGGAGGCCCTGATGGTACTAAAGTT 1851  
Qy 1741 CTGGTTACTCTGAAGCTGGCTGGTGTGGAGAAATCAGCCTTCTAGCAGCAGGAGA 1800  
Db 1852 CTGGTTACTCTGAAGCTGGCTGGTGTGGAGAAATCAGCCTTCTAGCAGCAGGAGA 1911  
Qy 1801 GGAACCCGTCGAACCTGCCAATGTGTGGCCGACCGGTTTGGCAATCTTTAACTCTAGAC 1860  
Db 1912 GGAACCCGTCGAACCTGCCAATGTGTGGCCGACCGGTTTGGCAATCTTTAACTCTAGAC 1971  
Qy 1861 AAAAGACCCCTCCAGAAATTTCTAGTCATTATCCAGATTTCTGAAGATCTCTCATGAAG 1920  
Db 1972 AAAAGACCCCTCCAGAAATTTCTAGTCATTATCCAGATTTCTGAAGATCTCTCATGAAG 2031  
Qy 1971 AAAGCCAGAGTCTTTTAAAGCAGAGGCTTAAGCCGACGAGCAACCCCTCCAGAAAT 1980  
Db 2032 AAAGCCAGAGTCTTTTAAAGCAGAGGCTTAAGCCGACGAGCAACCCCTCCAGAAAT 2091  
Qy 1981 GATCTTGCCCTCTCTCCACCGAAAGAGACACCAACTGTTTAAACTCTCTCTA 2040  
Db 2092 GATCTTGCCCTCTCTCCACCGAAAGAGACACCAACTGTTTAAACTCTCTCTA 2151  
Qy 2041 GGAGGCACAGAAAGCAAGTCTTGCAAGACTCTCAATTTGAAGCGAGAGCAAGCAGCT 2100  
Db 2152 GGAGGCACAGAAAGCAAGTCTTGCAAGACTCTCAATTTGAAGCGAGAGCAAGCAGCT 2211  
Qy 2101 CAGAAGAAAGAAATTTGAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160  
Db 2212 CAGAAGAAAGAAATTTGAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2271  
Qy 2161 AAAGAAATGAAGATAAAACAAAGAAATGAAGATAAGAGAAAGAAATGAAGATAAA 2220  
Db 2272 AAAGAAATGAAGATAAAACAAAGAAATGAAGATAAGAGAAAGAAATGAAGATAAA 2331  
Qy 2221 GATAAGGAAGAGAGCCAG 2280  
Db 2332 GATAAGGAAGAGAGCCAG 2391  
Qy 2281 ATTGAGTGGAG 2340  
Db 2392 ATTGAGTGGAG 2451  
Qy 2341 CGTCAATCACTTATTCAGCATGCTCTCTCTGCTGAGGCGGAGAGAGAGAGAGAGAG 2400  
Db 2452 CGTCAATCACTTATTCAGCATGCTCTCTCTGCTGAGGCGGAGAGAGAGAGAGAGAG 2511  
Qy 2401 ATTGAAGTCAAGAAAGGCTAAGCAATAA 2430  
Db 2512 ATTGAAGTCAAGAAAGGCTAAGCAATAA 2541

RESULT 2

AAS69653  
ID AAS69653 standard; cDNA; 2516 BP.  
XX  
XX  
AC AAS69653;  
XX  
XX 13-FEB-2002 (first entry)  
XX  
XX DNA encoding novel human diagnostic protein #5457.  
XX  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200175067-A2.  
XX  
XX 11-OCT-2001.  
XX

PF 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX P-PSDB; ASG05466.

XX New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity.

XX Claim 1; SEQ ID NO 5457; 103pp; English.

PS The invention relates to isolated polynucleotide (I) and polypeptide (II)

XX sequences. (I) is useful as hybridization probes, polymerase chain

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is

CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic

CC coding sequences of the invention. Note: The sequence data for this

CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 2516 BP; 1040 A; 548 C; 447 G; 481 T; 0 U; 0 Other;

Query Match 26.9%; Score 654.4; DB 5; Length 2516;

Best Local Similarity 99.1%; Pred. No. 1.3e-133;

Matches 658; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1767 GTTTGGAGAAATCAGCCTTTAGCAGCAGGAGGAGGAAACCGTGCATGCTGCTTGT 1826

Db 1853 GTCAGAAACCAACAGCCTTTAGCAGCAGGAGGAGGAAACCGTGCATGCTGCTTGT 1912

Qy 1827 GGGCCACGGGTTTGGCAATCTTTAACTAGACAAAGAGCCCTCCAGAAATTTCTAGT 1886

Db 1913 GGCCACGGGTTTGGCAATCTTTAACTAGACAAAGAGCCCTCCAGAAATTTCTAGT 1972

Qy 1887 GCATTATCCAGATTTCTGAAGGATCCTCATGAAGAGCCAGAGTGTCTTTAAAGCAGAA 1946

Db 1973 GCATTATCCAGATTTCTGAAGGATCCTCATGAAGAGCCAGAGTGTCTTTAAAGCAGAA 2032

Qy 1947 GGCTAAGACCGCAGAGCAACCCCTCCAGAAAGATCTTTGGCCCTCTCTTCCACCGAA 2006

Db 2033 GGCTAAGACCGCAGAGCAACCCCTCCAGAAAGATCTTTGGCCCTCTCTTCCACCGAA 2092

Qy 2007 AGAGAGACACCCCAACTGTTTAAACTCTCTAGGAGGAGCAGAGAAAGCAAGCTCTTGC 2066

Db 2093 AGAGAGACACCCCAACTGTTTAAACTCTCTAGGAGGAGCAGAGAAAGCAAGCTCTTGC 2152

Qy 2067 AAGACTACTCAAAATTGAAGCGAGAGCAAGCAGCTCAGAAGAAAGAAATTTCTGAAGGAGG 2126

Db 2153 AAGACTACTCAAAATTGAAGCGAGAGCAAGCAGCTCAGAAGAAAGAAATTTCTGAAGGAGG 2212

Qy 2127 AGAGGAAGAGGAAAGAAATGAAGATAAACAAGAAATGAAGATAAACAAGAAAGAA 2186

Db 2212 AGAGGAAGAGGAAAGAAATGAAGATAAACAAGAAATGAAGATAAACAAGAAAGAA 2272

Qy 2186 AGAGGAAGAGGAAAGAAATGAAGATAAACAAGAAATGAAGATAAACAAGAAAGAA 2242

Db 2272 AGAGGAAGAGGAAAGAAATGAAGATAAACAAGAAATGAAGATAAACAAGAAAGAA 2332

Qy 2242 AGAGGAAGAGGAAAGAAATGAAGATAAACAAGAAATGAAGATAAACAAGAAAGAA 2302

Db 2332 AGAGGAAGAGGAAAGAAATGAAGATAAACAAGAAATGAAGATAAACAAGAAAGAA 2392

Qy 2302 AGAGGAAGAGGAAAGAAATGAAGATAAACAAGAAATGAAGATAAACAAGAAAGAA 2362

Db 2392 AGAGGAAGAGGAAAGAAATGAAGATAAACAAGAAATGAAGATAAACAAGAAAGAA 2452

Db 2213 AGAGGAAAGGAAAGAAAGAAATCAAGATAAACAAAAAGAAATCAAGATAAACAAAAAGA 2272  
Qy 2187 AATGAGATTAAGGAAAGAAAGAAATGAAGATAAAGGATAAAGGAGAGAGCCAGAGAGAA 2246  
Db 2273 AATGAGATTAAGGAAAGAAAGAAATGAAGATAAAGGATAAAGGAGAGAGCCAGAGAGAA 2332  
Qy 2247 GCCACTGGACAGACCTGAATGTACAGCAAGTCCCTATTGCGAGTGGAGGAAGAACCCCACTC 2306  
Db 2333 GCCACTGGACAGACCTGAATGTACAGCAAGTCCCTATTGCGAGTGGAGGAAGAACCCCACTC 2392  
Qy 2307 AGTTAGAAGGACAGCTTTTACCAGAGGAGCTTCTCGTCAATCACTCATTTATCAGCATGGC 2366  
Db 2393 AGTTAGAAGGACAGCTTTTACCAGAGGAGCTTCTCGTCAATCACTCATTTATCAGCATGGC 2452  
Qy 2367 TCCTTCTGCTGAGGCGGAGAGAGGTTCTTACTATTGAAAGTCAAGAAAAGGCTAAGCA 2426  
Db 2453 TCCTTCTGCTGAGGCGGAGAGAGGTTCTTACTATTGAAAGTCAAGAAAAGGCTAAGCA 2512  
Qy 2427 ATAA 2430  
Db 2513 ATAA 2516  
RESULT 3  
ACN42631  
ID ACN42631 standard; cDNA; 4380 BP.  
XX ACN42631;  
AC ACN42631;  
XX 18-NOV-2004 (first entry)  
XX Human diagnostic and therapeutic polynucleotide SEQ ID NO:1506.  
XX ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;  
XX dithp.  
XX Homo sapiens.  
XX WO2004023973-A2.  
XX 25-MAR-2004.  
XX 12-SEP-2003; 2003WO-US028227.  
XX 12-SEP-2002; 2002US-0410259P.  
XX 12-SEP-2002; 2002US-0410260P.  
XX (INCY-) INCYTE CORP.  
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,  
XX Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;  
XX Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;  
XX Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;  
XX Peralta CH, Anderson SB, Rloux P, Shen EJ, Wu MC, Stuve LL;  
XX Lagace RB, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;  
XX Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
XX Patury S, Shi X, Suarez CJ;  
XX WPI; 2004-329368/30.  
XX P-PSDB; ABM83979.  
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
XX in diagnosing a condition, disease or disorder associated with human  
XX molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
XX in gene mapping.  
XX Claim 1; Page; 190pp; English.  
XX The invention relates to novel diagnostic and therapeutic polynucleotides  
XX selected from one of the 2722 sequences defined in the specification. A  
XX polynucleotide of the invention may have a use in gene therapy. The human  
XX diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
XX used to diagnose a particular condition, disease or disorder associated

CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithp polynucleotide of  
CC the invention. Note: The sequence data for this patent is not represented  
CC in the printed specification, but was obtained in electronic format  
CC directly from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
XX  
XX Sequence 4380 BP; 1048 A; 1233 C; 1318 G; 781 T; 0 U; 0 Other;  
Query Match 23.8%; Score 579; DB 13; Length 4380;  
Best Local Similarity 64.4%; Pred. No. 5.8e-117;  
Matches 867; Conservative 0; Mismatches 480; Indels 0; Gaps 0;  
Qy 617 TTCCAAACAGCATAGATTTCATACACAGATCGACTCTATCTCTGTGGCTCTTGTCTGTCA 676  
Db 1985 TTCCCAAGAGCATTGACCGCTGACCAACCTGATGTATGTCTATGGCTGTCTTCTGTGG 2044  
Qy 677 CTCCTGCTATTAACGTGAACTGCTGTTTATACCACTGCGCTCGTCTCCCAATACAA 736  
Db 2045 TGATGCCCTGGAAATGGAACTGTGGCTGATTCCTCCGCTGGGCTTCCCTACAGA 2104  
Qy 737 CGCGACACACATACACTACTGCTTATTGCGGACATCATATGTATATCATCTACTCTT 796  
Db 2105 CCCCAGACACATCCACCCTGCTGCTGATGATTAACCTATGCGACCTCATCTACTTCC 2164  
Qy 797 ATGATATGCTATTTATCCAGCCGACACTCCAGTTTGTAAAGAGGAGAGACATAATAGTG 856  
Db 2165 TGGACATCACCTGTGTCCAGACACGCTGCTGAGTGTTCAGAGGCGGGACATCATACG 2224  
Qy 857 ATTCAAAAGAGCTAAGGAAACACACAGACTCTTACAAAATTTCAAGTTGGATGTCGAT 916  
Db 2225 ACAAAGGACATGCGAAATAACTACTGAAGTCTCGCGCTTCAAGATGGACCTGCTCA 2284  
Qy 917 CAATAATACCATTTGATATTTGCTACTCTTCTTGGGTTTAAATCCAAATTTAGAGCAA 976  
Db 2285 GCCTCTGCCCTTGGATTTCTTATTTGAAAGTCTGCTGAAACCCCTCTCCGCTGC 2344  
Qy 977 ATAGGATGTTAAAGTACACTTCAATTTTTTGAATTTAATCATCACCTAGAGTCTATAATGG 1036  
Db 2345 CCGCTGTTTAAAGTACATGGCTTCTTCTGAGTTTAAACAGCCGCTTGAATCCATCTCA 2404  
Qy 1037 ACAAGCATATATCTACAGAGTTATTCGAAACAACTGGATCTTGTGTTTATTCGAC 1096  
Db 2405 GCAAAGCCTACGTGTACAGGGTTCATCAGGACCAAGCCCTTCTCTACAGCTGCAT 2464  
Qy 1097 TTAATGCTGCTTTTATTACTGGCTTCAAACTATGAAGGAATTTGGCACTACTAGATGG 1156  
Db 2465 TGAATTCCTGCTTTTATTACTGGGATCGGCTATCAGGGCTCGGCTCCACTACTGGG 2524  
Qy 1157 TGTATGATGGGGAAGAAACGAGTATCTGAGATGTTTATTATTGGGAGTTCGAATTTAA 1216  
Db 2525 TTTACGATGGCTGGGAAACAGTTATTTCTGCTGTCTTACTTCTGTGGAAGACCTCA 2584  
Qy 1217 TTACATTTGGTGGCTTCCAGAACCAAACTTTTATTTGAAATTTGTTTCACTCTGA 1276  
Db 2585 TCACCATCGGGGGCTGCTGACCCCAAGACACTCTTTGAAATTTGTTTCCAGCTGCTGA 2644  
Qy 1277 ATTTTCTGAGTTTCTGAGTTTCTCCAGTTTAAATTTGCTGAGATGAGAGATGATG 1336  
Db 2645 ATTATTTACGGGGCTCTTTGCTTTCTCTGATGATCGGACAGATGAGAGATGAGTAG 2704  
Qy 1337 GAGCAGCTACGCCAATCAGAACTACTTCCGCGCTGCTGATGATGACCAATTTGCTTACA 1396  
Db 2705 GGGCCGCCACCCCGGACAGACCTACTACCGCAGCTGCATGAGACAGACCGTGAAGTACA 2764  
Qy 1397 TGAACAATTTACTCCATTTCTTAACTTTGTCAAAAGGAGTTCCGACTTGGTATGATATA 1456  
Db 2765 TGAATTTCTTACAAGATCCCAAGTCCGTCAGAACCGGCTCAAGACCTGTCAGAGTACA 2824

617	QY	TTCCAAACAGCATAGATTTCAATACACAGATCGACTCTATCTCTGTGGCTTCTGCTTGTCTCA	676
782	Db	TTCCCCAGAGCATTTGACCGCTGACCAACCTGATGTATGTCTTATGGCTGTTCTTCGTGG	841
677	QY	CTCTGSCCTATAACTGGAACCTGCTGGTTTATACCACTGCGCCTCTGCTTCCCACATATCAA	736
842	Db	TGATGGCCTTGGAAATTGGAACTGTGTGGCTGANTCCCGTGGCTGGGCGCTTCCCCCTACAGA	901
737	QY	CGCGACAACAATACACTACTTGGCTTTATTCGGACATCATATGTGATATCATCTACCTTTT	796
902	Db	CCCCGACAACATCCACCACTGGCTGCTGATGGATTACCTATGCGACCTCATCTACTTCC	961
797	QY	ATGATATGCTATTTATTCAGCCACACTCCAGTTTGTATAAGAGAGAGAGACATTAATAGTGG	856
962	Db	TGGACATCACCGTGTTCAGACACGCTCGAGTTTGTCTCAGAGCGGGACATCAITACGG	1021
857	QY	ATTCAAATCAGCTAAGGAACAATAAGAGACTCTACAAAATTTTCAGTTGGATGTGCGAT	916
1022	Db	ACAAAAGACATGCGAAATAACTACCTGAAGTCTCGCGCTTCAAGATGGACCTGCTCA	1081
917	QY	CAATAATACCATTTGATATTTGCTACTCTCTCTTTGGGTTTAAATCCAAATGTTTAGAGCAA	976
1082	Db	GCTCTCGCCTTGGATTTTCTCTATTGGAAGTGGTGTGAACCCCTCTCCGCGTGC	1141
977	QY	ATAGGATGTTAAAGTACACTTCATTTTGTGAATTTAAATCATCACCTAGAGTCTATAATGG	1036
1142	Db	CCGCGTGTTTAAAGTACATGGCCTTCTTCAGTGTAAACAGCGCCTGGAATCCATCCTCA	1201
1037	QY	ACAAAGCATATATCTACAGAGTTATTCGAACAACCTGGATACTTGCCTGTTTATTTCTGCACA	1096
1202	Db	GCAAAAGCCTACGTGTACAGGGTTCATCAGGACCAACAGCTACCTTCTCTACAGCCTGCATT	1261
1097	QY	TTAATGCCCTGTGTTTATTACTGGCTTCAAACTATGAAAGAAATTTGGCACTACTAGATGGG	1156
1262	Db	TGAATTCCTGCTTTTATTACTGGCATTCGGCTTATCAGGGCCTCGGCTCACTACCTGGG	1321
1157	QY	TGTATGATGGGAAGAAACGAGTATCTGAGATGTTATTATTGGGCAGTTTCGAACCTTTAA	1216
1322	Db	TTTTACGATGGCTGGGAACAGTTTATTCGCTGTTTACTTGTGCTGAAGACCTCA	1381
1217	QY	TTACAAATTGGTGGCCTTCAGAAACCAAACTTTATTGAAATTTGTTTTTCAACTCTTGA	1276
1382	Db	TCACCATCGGGGGGTGCGCTGACCCCAACACACTCTTTGAAATTTGTCTTCCAGCTGCTGA	1441
1277	QY	ATTTTTTTTCTGGATTTTTTGTGTTCTCCAGTTTAAATTCGTGATGAGAGATGTGATGG	1336
1442	Db	ATATTTTACGGGCGTCTTTGTCTTCTGTGATGATCGGACAGATGAGAGATGTGGTAG	1501
1337	QY	GAGCAGCTACAGCCAATCAGAACTACTCTCCGGCCTGCTGATGATGATGACACCAATTCGCTACA	1396

Db	1502	GGGCGCGCACCGGGGACAGACCTTACTACCGCAGCTCATGGACAGCACCGGTGAAGTACA	1561
Qy	1397	TGAACAATTAATCTCCATTTCTTAAACTTGTGCAAAAGCGAGTTGGACATTGGTATGAATATA	1456
Db	1562	TGAATTTCTACAAGATCCCAAGTCCGTGCAGAACCGCGTCAAGACCTGGTACGAGTACA	1621
Qy	1457	CATGGGACTCTCAAGAATGCTAGATGAGTCTGATTTGCTTTAAGACCTTACCAACTACGG	1516
Db	1622	CCGTGGCACTCGCAAGGATGCTGGATGAGTCAGAGCTGATGGTGACAGCTTCCAGACAAGA	1681
Qy	1517	TCCAGTTAGCCCTCGCCATTGATGTGAACTTTCAGCATCATCAGCAAAAGTCGACTTGTTC	1576
Db	1682	TGCGGCTGGACCTCGCCATCGAGTGAATACAACATCGTTAGCAAAAGTCGACTCTTTC	1741
Qy	1577	AGGGTTGTGATACACAGATGATTTATGACATGTTGTCTAAGATTGAAATCCGGTCTCTATT	1636
Db	1742	AGGGCTGTGACCGGCAGATGATCTTTGACATGCTGAAGAGGCTTCGGCTCTGTTGTCTTACC	1801
Qy	1637	TGCTGTGTGACTTTGTCTGCAAAAAGGAGAAATTTGGCAAGGAAATCTATATCATCAAGC	1696
Db	1802	TGCCCAACGACTATGTGTGCAAGAGGGGAGATCGGCCGTGAGATGTCATCATCCAGG	1861
Qy	1697	ATGAGAAAGTCCAAAGTTCTTTGGAGGCCCTGATGAGTATAAAGTTCTGGTTACTCTGAAG	1756
Db	1862	CAGGGCAAGTGCAGGTCCTGGCGCGCCCTGATGGGAAATCTGTGCTGGTACGCTGAAAG	1921
Qy	1757	CTGGGTCGGTGTTTGGAGAAATCAGCCCTTCTAGCAGCAGGAGGAGAAACCGTCTGAAC	1816
Db	1922	CTGGATCTGTGTTTGGAGAAATAAGCTTGTCTGGCTTTGGGGCGGGNACCGGGCACGG	1981
Qy	1817	CCAATGTGTGTGGCCACGGGTTTGGCCAAATCTTTTAACTCTAGACAAAGAAGCCCTCAAG	1876
Db	1982	CCAACGTGTGTGGGCGACGGGTTTACCAACCTCTTTCATCTCTGGATAAGAAAGCACTG	2041
Qy	1877	AAATTTCTAGTGCATTATCCAGATTTCTGAAAGGATCCCTCATGAAGAAAGCCAGAGTGCTTT	1936
Db	2042	AGATTTTGGTGCATTATCTCTGAGTCTCAGAAAGTTACTCCGGAAGAAAGCCAGGGCATGC	2101
Qy	1937	TAAAGCAGAAGGCTTAAGACCGCAGAAG	1963
Db	2102	TGAGAAGCAACAATAAGCCCCAAGGAGG	2128

**RESULT 5**

**AAS91658**  
IP AAS91658 standard: cDNA: 3811 BP.

XX AAS91658:

XX  
DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #27462.

XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX  
OS Homo sapiens.

XX  
PN  
WO200175067-A2.

XX  
PD 11-OCT-2001.

XX  
PF  
30-MAR-2001: 2001WO-US008631.

XX  
PR 31-MAR-2000: 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.  
yy

PA (HYSE-) HYSEO INC.

XX  
PI  
Drmanac RT, Liu C, Tang YT:XX  
DR WPI; 2001-639362/73.

P-PSDB; ABG27471.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 1; SEQ ID NO 27462; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (I). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences)

Sequence 3811 BP; 812 A; 1093 C; 1102 G; 804 T; 0 U; 0 Other;



QY 1180 TATCTGAGATGTTATTTGGGAGTTCGAACCTTTAAATTACATTTGGTGGCCCTTCAGAA 1239  
DB 2549 TATATTCGCTGTACTACTTTGCTGTGAAGACCTCATCACCATCGGGGGCTGCTGAC 2608  
QY 1240 CCACAACTTTATTTGAAATTTCTTCAACTCTTTGAAATTTTCTTCTGGAGTTTGTG 1299  
DB 2609 CCCAGACACTCTTTGAAATTTCTTCAAGTCTGTAATTTTCCAGGGCGTCTTTGCT 2668  
QY 1300 TTCTCCAGTTTAAATTTGGTCAGATGAGATGTTGATTTGGAGCAGCTTACAGCCAAATCAGAAC 1359  
DB 2669 TTCTCTGTGATGATCGGACAGATGAGATGTTGGTAGGGCCGCCACCGGGGACAGACC 2728  
QY 1360 TACTTCCGGCTGATGATGACACCACTTGCCTACATGAACTTCTCAATCTTCTTAA 1419  
DB 2729 TACTACCCGAGCTGATGACACGACGCGTGAAGTACATGAAATTTCTCAAGATCCCAAG 2788  
QY 1420 CTTGTGCAAAAGCGAGTTTCGGACTTGGTATGATATATACATGGAGCTCTCAAGAAATGCTA 1479  
DB 2789 TCCGTGCAAGACCGCTCAGACCTTGTGACGATGATACCTGGCATCTCGAAGGATGCTG 2848  
QY 1480 GATGATCTGATTTGCTTAAAGACCTTACCAACTACGGTCCAGTTAGCCCTCGCCATGAT 1539  
DB 2849 GATGATCAGAGCTGATGTCGAGCTTCCAGACAAGATCGGCTGAGCTCGCCATGAC 2908  
QY 1540 GTGAACCTTCCAGATCATCAGCAAGTGCATTTTCAAGGGTTGTGATACACAGATGAT 1599  
DB 2909 GTGAACCTTCAACATCTGTAGCAAGTGCATCTTTTCAGGGCTGTGACCGGCAGATGATC 2968  
QY 1600 TATGATCTTGTCTAAGATTGAATCCGTTCTCTATTTTCCCTGGTGACTTTGTCTGCAAA 1659  
DB 2969 TTTGACATGCTGAAGAGCTTCGCTCTGTTTGTCTACCTGCCCAAGCATATGTGTGCAAG 3028  
QY 1660 AAGGAGAAATTTGGCAAGAAATGTATATCATCAAGCATGGAGAGTCCAAAGTTCTTGG 1719  
DB 3029 AAGGGGAGATCGGCGGTGAGATGTACATCATCCAGGCAAGGCAAGTGCAGTCTTGGGC 3088  
QY 1720 GGCCCTGATGTTACTAAAGTTCTGTTACTCTGAAAGCTGGTGGTGGTGGAGAAATC 1779  
DB 3089 GGCCCTGATGGAAATCTGTGCTGTGCTGACGCTGAAAGCTGATCTGTGTTGGAGAAATA 3148  
QY 1780 AGCTTCTAGCAGCAGGAGGAGAAACCGTGCAGTGCATGTGGTGGCCACCGGGTTT 1839  
DB 3149 AGCTTCTGCTGTGTTGGGGGGGAGGACCGGCGCACGCTGAGATGAGATTTGGTGCATATCTGAG 3208  
QY 1840 GCCAATCTTTTAACTCTAGACAAAAGACCCCTCCAAAGAAATTTAGTGCATTTATCCAGAT 1899  
DB 3209 ACCAATCTTTCATCTCGATAAGAGGACCTGATGAGATTTGGTGCATATCTGAG 3268  
QY 1900 TCTGAAAGATCTTCATGAAGAGCCAGAGTGTCTTTTAAAGCAGAGAGGCTTAAGACCGCA 1959  
DB 3269 TCTCAGAAATTTACTCCGGAAGAAAGCCAGGCGCATGCTGAGAAGCAACAATAAGCCCAAG 3328  
QY 1960 GAAG 1963  
DB 3329 GAGG 3332

RESULT 6  
ADB53355  
ID ADB53355 standard; DNA; 4238 BP.  
XX AC ADB53355;  
XX AC  
XX AC  
DT 04-DEC-2003 (first entry)  
XX DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3897.  
XX DE  
XX DE toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;  
XX DE toxicity marker; toxicity progression; drug screening;  
XX DE primary rat hepatocyte toxicity modelling; gene; ds.  
XX OS Rattus norvegicus.  
XX

PN WO2003065993-A2.  
XX  
PD 14-AUG-2003.  
XX  
PF 04-FEB-2003; 2003WO-US003482.  
XX  
PR 04-FEB-2002; 2002US-0353171P.  
PR 13-MAR-2002; 2002US-0363534P.  
PR 08-APR-2002; 2002US-0370248P.  
PR 10-APR-2002; 2002US-0371134P.  
PR 10-APR-2002; 2002US-0371135P.  
PR 10-APR-2002; 2002US-0371150P.  
PR 11-APR-2002; 2002US-0371413P.  
PR 19-APR-2002; 2002US-0373601P.  
PR 19-APR-2002; 2002US-0373602P.  
PR 22-APR-2002; 2002US-0374139P.  
PR 08-MAY-2002; 2002US-0378370P.  
PR 09-MAY-2002; 2002US-0378652P.  
PR 09-MAY-2002; 2002US-0378653P.  
PR 09-JUL-2002; 2002US-0394230P.  
PR 09-JUL-2002; 2002US-0394253P.  
PR 04-SEP-2002; 2002US-0407688P.  
PR 28-JAN-2003; 2003US-0442900P.  
XX (GENE-) GENE LOGIC INC.  
XX Mendrick D; Porter M, Johnson K, Higgs B, Castle A, Orr M;  
PI Elashoff M;  
XX  
XX WPI; 2003-731472/69.  
XX  
PT Determining if a compound induces a toxic effect on a tissue or cell, for  
PT identifying hepatotoxic compounds, comprises comparing a gene expression  
PT profile of a tissue or cell sample to a database of Tox mean and non-Tox  
PT mean values.  
XX  
XX Claim 44; SEQ ID NO 3897; 874pp; English.  
XX  
CC The present invention describes a method for determining whether a  
CC compound induces a toxic effect on a tissue or cell. The method comprises  
CC preparing a gene expression profile of a tissue or cell sample exposed to  
CC the compound, and comparing the gene expression profile to a database  
CC comprising data or information on the Tox mean and non-Tox mean value.  
CC The method is useful for predicting or identifying at least one toxic  
CC effect, particularly hepatotoxicity, of a test or unknown compound. The  
CC genes listed in the specification are useful as diagnostic or toxicity  
CC markers for the prediction or identification of the physiological state  
CC of tissue or cell sample that has been exposed to a compound, or to  
CC identify or predict the toxic effects of a compound or an agent. These  
CC may also be used as markers for monitoring toxicity progression or for  
CC drug screening. The present sequence represents a primary rat hepatocyte  
CC toxicity modelling related gene sequence from the present invention.  
XX  
XX Sequence 4238 BP; 1129 A; 1107 C; 1313 G; 689 T; 0 U; 0 Other;  
SQ  
Query Match 23.4%; Score 569.6; DB 10; Length 4238;  
Best Local Similarity 64.6%; Pred. No. 6.7e-115;  
Matches 848; Conservative 0; Mismatches 464; Indels 0; Gaps 0;  
QY 617 TTCCAAACAGCATAGATTTCATACACAGATCGACTCTATCTCTGTGGCTCTTGTGTCA 676  
DB 2277 TCCCCCAGAGCATCGACCCACTGACCAACCTCATGTATCATCTGTGGCTGTCTTCTGGTGG 2336  
QY 677 CTCTTGCTTATACTGGAACCTGCTGTTTATACACTGGCGCTCGTCTCCCATATCAAA 736  
DB 2337 TGCTGGCTGGAACCTGGAACCTGCTGCTGATTCCTGTGCGCTGGCGCTTCCCGTACCAGC 2396  
QY 737 CCGCAGACAACATACACTTACTGCTTATTTGGGACATCATATGTATCATCTACCTTT 796  
DB 2397 GGGCAGACAACATCCACTCTGGCTGCTCATGTGACTTCTGTGACATTCATCTACCTCC 2456  
QY 797 ATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTAAAGAGGAGGAGACATAATAGTGG 856

Db 2457 TGGACATCACCGTGTCCAGATGGTCTCCAGTTTGTCAAAGGCGGGACATCATACAG 2516  
Qy 857 ATTCAATGAGCTAAGAAACACTACAGGACTTCTACAAAATTTTCAGTTGGATGTGCGAT 916  
Db 2517 ATAAGAGGAGATGCGTAATATTTACCTGAAGTCTCAACGATTTAAGATGGACTTGCTCT 2576  
Qy 917 CAATAATACCAATTGATATTGCTTACCTCTCTTTGGGTTTAAATCCAATGTTAGAGCAA 976  
Db 2577 GCCTTTTGCCTTTGGATTTCTCTACTTGAAACTTGGCGTGAACCCCTTCTTCGCGTGC 2636  
Qy 977 ATAGGATGTTAAAGTACACTTCAATTTTGAATTTAATCATCACCTAGAGTCTATAATGG 1036  
Db 2637 CCGCTCGCTGAAGTACATGGCTTCTTTGAGTTTAAATACCGTCTGGAAGCCATCTCA 2696  
Qy 1037 ACAAAGCATATCTACAGAGTTATTCGAACAACCTGATACTTGTGTTTATTTCTGCACA 1096  
Db 2697 GCAAAGCCTACGTTTACAGGGTTATCAGGAGTATCAGGACCCGCTTACCTGCTGTATAGCTTGCATC 2756  
Qy 1097 TTAATGCTGCTGTTTATTACTGGCTTCAAACTATGAAGAAATGGCACTACTAGATGG 1156  
Db 2757 TCAACTCTGCTTTACTTGGGCTGGGCTTCCAGGCGATCGGTTCCACTACTGGG 2816  
Qy 1157 TGTATGATGGGAGGAAACGAGTATCTGAGATGTTTATTATGGCGAGTTTCAACTTTAA 1216  
Db 2817 TTTATGACGGCTGGGGAACAGCTTACATTCGATGCTACTTGGCTGTGAAAACCTCA 2876  
Qy 1217 TTACCATTTGGCTTCCAGAACCAAACTTTATTTGAATTTGTTTCAACTCTTGA 1276  
Db 2877 TCACCATCGGAGGACTGCCCGACCCCGACGCTCTTTGAGATCGTCTCCAGCTGCTGA 2936  
Qy 1277 ATTTTCTTCTGGAGTTTGTGTTCTCCAGTTTAAATGTCAGATGAGAGATGTGATTG 1336  
Db 2937 ATTATTTTACAGTGCTTCTGCTTCTCTGTGATGATGGACAGATGAGAGATGTGGTG 2996  
Qy 1337 GAGCAGCTACAGCAATCAGAACTACTTCCGCGCTGTCATGATGACACCAATTTGCCCTACA 1396  
Db 2997 GGGCGCGCACGGCAGCAGCTACTTACCGAGCTGTCATGGACAGCAGCGTGAAGTACA 3056  
Qy 1397 TGAACAACTACTCATCTTAACTTGTGCAAAAGGAGTTCCGACTTGGTATGAATATA 1456  
Db 3057 TGAACCTTCTAAGATCCCCAGGCTGTGTGCAAGACCGCGTCAAGACCTGGTGTACGAATACA 3116  
Qy 1457 CATGGAGCTCTCAAGAACTCTAGATGAGTGTGATTTGCTTAAAGCCCTACCAACTACGG 1516  
Db 3117 CTTGGCACTCAAGCAATGCTGATGAGTTCAGAGCTGATGGTTTCAGCTTCCGGAAGA 3176  
Qy 1517 TCCAGTTAGCCCTCGCCATTGATGTGAATTTTCAGCATCATCAAGAAAGTTCGACTTGTCA 1576  
Db 3177 TGGCTCTGGACCTGGCCATTGACGTAAACTTACAACATTTGTCAGAAAGTGGCGCTCTTCC 3236  
Qy 1577 AGSGTTGTGATACACAGATGATTTATGACATGTTGTGAAGTTGAATGAAATCGGTTCTATT 1636  
Db 3237 AGGGCTGCGACCGGAGATGATCTTCGACATGCTCAAGCGACTTCGCTCAGTCTGCTACC 3296  
Qy 1637 TGCTGTGTGATTTGTCTCAAAAAGGAGAAATTTGCAAGGAAATGTATATCATCAAGC 1696  
Db 3297 TACCCATGACTATGTGTGCAAGAGGGGAGATTTGGCCGAGAGATGTATATATATCCAGG 3356  
Qy 1697 ATGGAGAAGTCCAAGTTCTTTGGAGGCCCTGATGGTACTAAAGTTCTGGTTACTTCTGAAAG 1756  
Db 3357 CGGGGCAAGTGCAGGTGCTGGCGGCCAGATGGAAGGCTGCTCGGTGACACTCAAAG 3416  
Qy 1757 CTGGGTGGTGTGAGAAATCAGCCTTCTACAGCAGAGAGAGGAAACCGTTCGAACTG 1816  
Db 3417 CCGGATCGGTTTGGAGAGATAAGCTTGTGCTGTGCGGGCGGTAACAGCGCACGG 3476  
Qy 1817 CCAATGTGGTGGCCACGGGTTTGGCAATCTTTTAACTCTAGACAAAAGACCCCTCCAAG 1876  
Db 3477 CCAATGTGGTGGCCACGGCTTCAACCAATCTTCTTCACTTGGATAGAAGGACTTGAATG 3536  
Qy 1877 AAATCTAGTGCAATATCCAGATTTCTGAAAGGATTCCTCATGAAAGAACGCCAG 1928

Db 3537 AGATTTTGGTGCATTACCTGAATCTCAGAAGCTGCTCCGGAAGAGGCCAG 3588  
RESULT 7  
ID ADS64556 standard; DNA; 3236 BP.  
XX  
AC ADS64556;  
XX  
DT 16-DEC-2004 (first entry)  
XX  
DE Norway rat cyclic nucleotide-gated ion channel 4.3 (CNG4.3) DNA.  
XX  
KW cyclic nucleotide concentration; screening;  
KW cyclic nucleotide-gated ion channel 4.3; CNG4.3; ds.  
XX  
OS Rattus norvegicus.  
XX  
PN W02004083803-A2.  
XX  
XX 30-SEP-2004.  
XX  
PF 06-MAR-2004; 2004WO-BP002317.  
XX  
PR 18-MAR-2003; 2003DE-01011769.  
XX  
XX (FARB ) BAYER HEALTHCARE AG.  
XX  
PI Wunder F;  
XX  
DR WPI; 2004-728498/71.  
XX  
PT Determining intracellular concentration of cyclic nucleotides, useful for  
PT identifying, e.g. receptor ligands and enzyme inhibitors, comprises using  
PT cells that express a cyclic nucleotide activated ion channel and a  
PT photoprotein.  
XX  
PS Example; SEQ ID NO 2; 20pp; German.  
XX  
CC The invention relates to a novel method for determining the intracellular  
CC concentration of cyclic nucleotides. The method comprises preparing a  
CC cell that expresses a CNG (cyclic nucleotide-activated) ion channel  
CC together with a photoprotein and detecting the intracellular  
CC concentration of cyclic nucleotides from the luminescent signal of the  
CC photoprotein. The method may be used to screen for receptor ligands and  
CC modulators of phosphodiesterase, guanylate cyclase or nitric oxide  
CC synthase, which would be potentially useful as pharmaceuticals. The  
CC method is suitable for high throughput screening, does not require  
CC radioactive tracers, has a high signal-to-noise ratio, is very quick,  
CC highly sensitive and inexpensive. The current sequence is that of the  
CC Norway rat cyclic nucleotide-gated ion channel 4.3 (CNG4.3) DNA of the  
CC invention.  
XX  
SQ Sequence 3236 BP; 780 A; 962 C; 903 G; 591 T; 0 U; 0 Other;  
Query Match 23.4%; Score 568; DB 13; Length 3236;  
Best Local Similarity 64.6%; Pred. No. 1.4e-114;  
Matches 847; Conservative 0; Mismatches 465; Indels 0; Gaps 0;  
Qy 617 TTCCAAACAGCATAGATTTCATACAGATTCGACTCTATCTCTGTGGCTTCTTGTGTC 676  
Db 1211 TCCCCCAGAGCATGACCCACTGACCACTCATGTACATCTGTGGCTGTTCTTGTGG 1270  
Qy 677 CTCCTTGCCTATTAACCTGGAACCTGCTGTTTATACCACTGGCTCTCTCCATATCAA 736  
Db 1271 TCGTGGCTTGGAACTGGAACCTGCTGGCTGATTCCTGTGGCTGGGCTTCCCGTACC 1330  
Qy 737 CGCGACAGAACATACACTACTGCTGCTTATTCGCGCATCATATGTGATATCATCTT 796  
Db 1331 GGGCAGACAAATCCACCTCTGGCTGCTCATGGAATCTTGTGGCACTTCACTACCTCC 1390  
Qy 797 ATGATATGCTATTTATCCAGCCCACTCCAGTTCCTGTTTGAAGAGAGAGACATAATAGTGG 856



Db 143 ACAACCGCTGCGAGCTCCTGTTATAAATGAGTATGCGGATGCCAGCTACACAACTGG 202  
Qy 407 TGAAGAAGTCCGCTCAAGACAGCCCTCTACAGAAAAAGTTGGTAGAGGAGATCTCT 466  
Db 203 TGAAGAAGTCCGCTCAAGACAGCCCTCTACAGAAAAAGTTGGTAGAGGAGATCTCT 262  
Qy 467 CCTCACCAGGAGCCAGCCCAAACTGCAAGCCCGCTGTACCAACAGTAAAGAAA 526  
Db 263 CCTCACCAGGAGCCAGCCCAAACTGCAAGCCCGCTGTACCAACAGTAAAGAAA 322  
Qy 527 GCGATGATAAGCCCAAGAACATTTACTACAGGCTGTTGTTGTTCAAAAGTCAAAAGATGC 586  
Db 323 GCGATGATAAGCCCAAGAACATTTACTACAGGCTGTTGTTGTTCAAAAGTCAAAAGATGC 382  
Qy 587 CTTTAAACAGTACTTAAAGGGAATTAACCTTCAACACAGCATAGATTCAACACAGATC 646  
Db 383 CTTTAAACAGGATCTTAAAGCGGAATTAACCTTCAACACAGCATAGATTCAACACAGATC 442  
Qy 647 GACTCTATCTCCTGTGGCTCTTGTCTGCTCACTTGTGCTATACTGGAAGTCTGGTTTA 706  
Db 443 GACTCTATCTCCTGTGGCTCTTGTCTGCTCACTTGTGCTATACTGGAAGTCTGGTTTA 502  
Qy 707 TACCACCTGCGCTCGTCTTCCCATATCAAAACCGCAGACAACTACTACTGCTTATTG 766  
Db 503 TACCACCTGCGCTCGTCTTCCCATATCAAAACCGCAGACAACTACTACTGCTTATTG 562  
Qy 767 CGGACATCATATGATGATATCATCTACCTTTTATGATGCTATTATCCAGCCAGACTCC 826  
Db 563 CGGACATCATATGATGATATCATCTACCTTTTATGATGCTATTATCCAGCCAGACTCC 622  
Qy 827 AGTTTGTAGAGGAGGAGACATAATA 852  
Db 623 AGTTTGTAGAGGAGGAGACATAATA 648

RESULT 9

AA576184/c  
ID AA576184 standard; cDNA; 2244 BP.  
XX  
AC AA576184;  
XX  
XX  
DT 13-FEB-2002 (first entry)  
XX  
XX DNA encoding novel human diagnostic protein #11988.  
XX  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US008631.  
XX  
XX 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Drmanac RT, Liu C, Tang YT;  
XX  
XX WPI; 2001-639362/73.  
DR P-PSDB; ABG11997.  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
PS Claim 1; SEQ ID NO 11988; 103pp; English.

XX  
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AA564197-AA594564 represent novel human diagnostic  
CC coding sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 2244 BP; 463 A; 592 C; 469 G; 720 T; 0 U; 0 Other;  
Query Match 21.3%; Score 518; DB 5; Length 2244;  
Best Local Similarity 94.7%; Pred. No. 1-2e-103;  
Matches 536; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
Qy 287 GAACAGTGCAGCAGAGAAAGAAATGGACCCCGGAAAGAGGTCCAAACAGCCCAAA 346  
Db 2162 GCAAACTATCACAGGACAGAAACCCAAACACCGCATGTCTCACAAACAGCCCAAA 2103  
Qy 347 ACAACCGGCTCGAGCTCCTGTTATAAATGAGTATGCCGATGCCAGCTACCAACCTGG 406  
Db 2102 ACAACCGGCTCGAGCTCCTGTTATAAATGAGTATGCCGATGCCAGCTACCAACCTGG 2043  
Qy 407 TGAAGAAGTCCGCTCAAGAACAGCCCTCTACAAAGAAAAAGTTGGTAGAGGAGATCTCT 466  
Db 2042 TGAAGAAGTCCGCTCAAGAACAGCCCTCTACAGAAAAAGTTGGTAGAGGAGATCTCT 1983  
Qy 467 CTTACCCGAGCCAGCCCAAACTGCAAGCCCAACCGCTGTACCAACAGTAAAGAAA 526  
Db 1982 CTTACCCGAGCCAGCCCAAACTGCAAGCCCAACCGCTGTACCAACAGTAAAGAAA 1923  
Qy 527 GCGATGATAAGCCCAAGACAGACATTTACTACAGGCTGTTGGTTCAAGTCAAAAGATGC 586  
Db 1922 GCGATGATAAGCCCAAGACAGACATTTACTACAGGCTGTTGGTTCAAGTCAAAAGATGC 1863  
Qy 587 CTTTAAACAGGATCTTAAAGCGAATTTAAACTTCCAAACAGCATAGATTCAACAGATC 646  
Db 1862 CTTTAAACAGGATCTTAAAGCGAATTTAAACTTCCAAACAGCATAGATTCAACAGATC 1803  
Qy 647 GACTCTATCTCCTGTGGCTCTTGTGTCACCTCTTGCCTATTAACCTGGAATCTGCTGTTTA 706  
Db 1802 GACTCTATCTCCTGTGGCTCTTGTGTCACCTCTTGCCTATTAACCTGGAATCTGCTGTTTA 1743  
Qy 707 TACCACCTGCGCTCGCTCTTCCCATATCAACCGCAGACAACTACTACTGCTTATTG 766  
Db 1742 TACCACCTGCGCTCGCTCTTCCCATATCAACCGCAGACAACTACTACTGCTTATTG 1683  
Qy 767 CGGACATCATATGATATCATCTACCTTTTATGATATGCTATTATCCAGCCAGACTCC 826  
Db 1682 CGGACATCATATGATATCATCTACCTTTTATGATATGCTATTATCCAGCCAGACTCC 1623  
Qy 827 AGTTTGTAGAGGAGGAGACATAATA 852  
Db 1622 AGTTTGTAGAGGAGGAGACATAATA 1597

RESULT 10

ABL19457  
ID ABL19457 standard; DNA; 3275 BP.

XX ABL19457;  
AC  
XX 26-MAR-2002 (first entry)  
DT  
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 9844.  
DE  
XX Drosophila; developmental biology; cell signalling; insecticide;  
KW  
XX pharmaceutical; gene; ds.  
KW  
XX Drosophila melanogaster.  
OS  
XX WO200171042-A2.  
PN  
XX 27-SEP-2001.  
PD  
XX 23-MAR-2001; 2001WO-US009231.  
PF  
XX 23-MAR-2000; 2000US-0191637P.  
PR  
XX 11-JUL-2000; 2000US-00614150.  
PT  
XX (PBEK) PE CORP NY.  
PA  
XX Venter JC, Adams M, Li PWD, Myers EW;  
PI  
XX WPI; 2001-656860/75.  
DR  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
XX genes from Drosophila and for elucidating cell signaling and cell-cell  
XX interactions.  
XX  
XX Claim 1; SEQ ID NO 9844; 21pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
XX capable of detecting 1000 or more genes from Drosophila. The invention is  
XX useful in developmental biology and in elucidating cell signalling and  
XX cell-cell interactions in higher eukaryotes for the development of  
XX insecticides, therapeutics and pharmaceutical drugs. The invention  
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-  
XX ABB72072). The sequence data for this patent did not form part of the  
XX printed specification, but was obtained in electronic format directly  
XX from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 3275 BP; 843 A; 849 C; 873 G; 710 T; 0 U; 0 Other;  
XX  
XX Query Match 9.2%; Score 223; DB 4; Length 3275;  
XX Best Local Similarity 48.7%; Pred.No. 9.4e-39;  
XX Matches 635; Conservative 0; Mismatches 665; Indels 3; Gaps 1;  
XX  
XX 650 TCTATCTCTGGCTCTTGGCTTGTCTCACTCTTGCCTATAACTGGAACTGCTGGTTATAC 709  
XX 1552 TCTACATCTCTGGCTATGCGTGTGTATCGCTATCGTTTCTTATACCGCTGGGTATCC 1611  
XX 710 CACTGCGCTCTCTTCCCATATCAAAACCGCAGAACACATACATCTGGCTTATGCGG 769  
XX 1612 CGCTGCGCTCGTCTTCCCTTCAACCAAGGAGAACCAATATCTGCTGGCTGCG 1671  
XX 770 ACATCATATGATATCATCTACCTTTATGATATGCTATTTATCCAGCCAGACTCCAGT 829  
XX 1672 ACTTTGCGCTGACATCATATATCTACTGGAATGTGTCTCTTTAAACATCGGGTATGT 1731  
XX 830 TTGTAAGAGGAGGAGACATAATAGTGGATTCAATGAGCTAAGGAAACACATACAGACTT 889  
XX 1732 ACCTTTTGGAGGATCTGGGTGAAACAAACAGAACCTCACCAGAAAGAACTACATCGGA 1791  
XX 890 CTACAAATTTAGTGGATGTCGCATCAATAATACCAATTTGATATTTGCTTCTTCT 949  
XX 1792 AACTGCAGTTTAAAGTGGATCTGCGGCCCTCTTCCGCTGGAGCTATTGACTTAAAC 1851  
XX 950 TTGGTTTAAATCCCAAT---GTTTATAGCAAAATAGGATGTTAAAGTACACTTCATTTT 1006  
XX 1852 TCGGAACACAGGCGGTTTGGTTGCGTTTTCCTTTTCAAGGTTCTTTAAGATTCAGAGCTTCTGG 1911

RESULT 11

ADD93243

ID ADD93243 standard; cDNA; 2500 BP.

XX ADD93243;

AC ADD93243;

XX 29-JAN-2004 (first entry)

QY 1007 AATTAAATCATCCTAGAGTCTATAATGGACAAAGCATATATCTACAGAGTTATTCGAA 1066  
DB |||||  
DB 1912 AAGTGTTCGGCTTTTGGATCGAGTCATATCTTCTCCGCACTTTTTCGAGTGGCCAAA 1971  
QY 1067 CAATCGGATCTCTGCTTTTATTCTGCACATTAATGCTGTGTATTATTACTGGGTTCAA 1126  
DB |||||  
DB 1972 CCCTAACCTACATGCTCTACATGATCCACATCAGGCTGCTCTGTACTACGCTATAGT 2031  
QY 1127 ACTATGAAGGAATTTGGCACTACTAGATGGGTGTATGATGGGGAAGAAACAGATATCTGA 1186  
DB |||||  
DB 2032 ACTACAGGCTCTGGACAGATCTTGGGTCTTCAGCGGCAAGGGCATCCCTATGTAA 2091  
QY 1187 GATGTATTATTGGGCACTTTCGAATTTAAATTAATCAATGGTGGGCTTCCAGAACCAAAA 1246  
DB |||||  
DB 2092 GGTGCTTTGCTTTTCCCAACCAAGACGCGCACTTCGATAGGAAACAAACCCCAAGCGGAAC 2151  
QY 1247 CTTTATTGAAATTTGTTTCAACTCTTGAATTTTCTGGAGTTTCTGTTGTTCTCCA 1306  
DB |||||  
DB 2152 GTCAGGAGATGATGCTCTTCATGACGGTGGCTGGCTAAAGGGGCTCTTTGTGTCGCTC 2211  
QY 1307 GTTTAAATTTGGTCAGATGAGATGATGATGGAGCAGCTACAGCAATCAGAACTACTTCC 1366  
DB |||||  
DB 2212 TGCTTATCGTTCAGATCAGGATATCATCTCGACGCCACTCGGATTAAGCATGATATC 2271  
QY 1367 GCGCTCTGATGATGACACCATTCCTCATATGAAACAAATTAATCTTAACTTAACTTGGC 1426  
DB |||||  
DB 2272 GCCAGCTGGAGATGAGACACTGGAGTACATGCGACGCTCAATCTCTCGCAGGAGTGC 2331  
QY 1427 AAAAGCAGTTGCGACTTGGTATGAATATACATGGACTCTCAAGATGCTAGATGAT 1486  
DB |||||  
DB 2332 AGTCAGGGTCAAAATGTGGTTCAGTTTACATGGGAGCAGCGCACTTTGGATGAAT 2391  
QY 1487 CTGATTTGCTTAAAGACCTTACCAACTCGGTCCAGTTAGCCCTCGCCATGATGTGAAT 1546  
DB |||||  
DB 2392 CCAACATATTGGATGCTTTGCGCATCAATTTGAAACCGGATATCGCATCTCCGTGCA 2451  
QY 1547 TCAGCATCATCAGCAAAAGTCGACTTGTTCAAAGGTTGTGATACACAGATGATTTATGCA 1606  
DB |||||  
DB 2452 TCCAAACGCTCTCCAAGGTGCAACTCTTTGCTGATTTGGAGAGGCTTTACTCAGAGATC 2511  
QY 1607 TGTGCTAAGATTGAAATCGTTCCTATTTGCTGCTGAGCTTTGTCTGCAAAAAGGAG 1666  
DB |||||  
DB 2512 TGGTTCTAAAACCTAAGGCGAGTCACATTTTTCAGGAGATTTCTGTTTGGCCGCAAGGCG 2571  
QY 1667 AAATTGGCAAGAAATGTATATCATCAAGCATGAGAAAGTCCAAAGTTCTTGGAGCCCTG 1726  
DB |||||  
DB 2572 AAGTGGCAGAGATGTATATCTGTAACCTGGGACAGGTTCAAGTATGGTGTGCTCTA 2631  
QY 1727 ATGTTACTTAAAGTTCTGGTTACTCTGAAAGCTGGGTGGTGTGTTGGAGAAATCAGCCTTC 1786  
DB |||||  
DB 2632 GTAGCGATGTAGTCTGGCACTCTAACCGAAGGTTCGCTGTTCCGGGAGATCAGTCTGC 2691  
QY 1787 TAGCAGCAGGAGGAGGAAACCGTCACTGCAATGTCGATGTTGGGCCCAACGGGTTTGCCTA 1846  
DB |||||  
DB 2692 TGGGAATAAATGGAGCGGATCGCAGAAACAGAGATGTCGATCCAAAGGCTACTCCAAAC 2751  
QY 1847 TTTTAACTCTAGACAAAGAACCCCTCCAAAGAAATTTCTAGTGCATTATCCAGATTTCTGAA 1906  
DB |||||  
DB 2752 TGTTCGCTGCTGCCAAATCGGATTTAAACGAGGTCATTGCTCTATATCCACGGGCCAGG 2811  
QY 1907 GGATCTCATGAAGAAAGCCAGAGTGTCTTTTAAAGCAGAAAGGC 1949  
DB |||||  
DB 2812 CGATTCTCAAAAGCGTCTGCTCAGCTTAATGCCGAAAAATGC 2854

XX	Cyclic nucleotide gated channel alpha 1 coding sequence.	
DE	ss; gene; cyclic nucleotide gated channel alpha 1 ;	
XX	central nervous system; CNS; eye; blood-brain barrier;	
KW	blood-retina barrier; angiogenesis ; revascularisation;	
KW	retinal pigment epithelium; RPE; neurosensory retina ; choroidea ;	
KW	age-related macular degeneration; AMD; diabetic retinopathy;	
KW	Alzheimer's disease; Parkinson's disease; depression; bipolar disorder;	
KW	schizophrenia; amnesia; headache; stroke; insomnia; alcohol abuse;	
KW	anxiety; chronic pain; retinal blastoma; primary retinal detachment .	
XX	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	CDS	25..2097
FT		/*tag= a
FT		/product= "Cyclic nucleotide gated channel alpha 1"
XX		
PN	W02003087368-A2.	
XX		
PD	23-OCT-2003.	
XX		
XX	16-APR-2003; 2003WO-EP004003.	
XX		
PR	18-APR-2002; 2002EP-00008761.	
PR	05-DEC-2002; 2002US-0431173P.	
XX		
PA	(LYNK-) LYNKEUS BIO TECH GMBH.	
XX		
PI	Drumm K, Schloer SH, Goehring F;	
XX		
DR	WPI; 2003-845328/78.	
DR	P-PSDB; ADD93244.	
XX		
PT	Treating central nervous system and/or eye disorders comprises	
PT	administering to a subject a composition comprising a compound that	
PT	modulates a target gene or gene product, outside the blood-brain and/or	
PT	blood-retina barriers.	
XX		
PS	Claim 19; SEQ ID NO 1; 91pp; English.	
XX		
CC	This sequence encodes the human cyclic nucleotide gated channel alpha 1	
CC	protein. This cDNA may be targeted in the method of the invention for	
CC	treating a disorder of the central nervous system (CNS) and/or the eye.	
CC	The method comprises administering to a subject a composition comprising	
CC	a compound capable of modulating a target gene or gene product in a	
CC	therapeutic amount, where the composition is administered outside the	
CC	blood-brain and/or the blood-retina barriers. The composition is in a	
CC	designed form to be introduced into the cells or tissue of the CNS or eye	
CC	by a suitable carrier, characterized by the application occurring outside	
CC	the blood-brain or blood-retina barriers. It is also designed for	
CC	systemic administration or for administration by iontophoresis, or for	
CC	retrobulbar application or as eye drops. The compound, nucleic acid	
CC	molecule or vector is useful for the preparation of a composition for	
CC	treating, preventing and/or delaying a disorder of the CNS and/or the	
CC	eye, e.g. related to angiogenesis and/or neovascularisation, retinal	
CC	pigment epithelium (RPE), neurosensory retina and/or choroidea and wet	
CC	age-related macular degeneration (AMD) or diabetic retinopathy. The	
CC	compound may also be used as a lead compound in drug discovery and	
CC	preparation of drugs or prodrugs. The nucleic acid molecule and	
CC	polypeptide are also used for the validation of test substances, lead	
CC	compounds, drugs and prodrugs for the treatment of the disorder mentioned	
CC	above or for the identification and isolation of downstream genes, which	
CC	respond to modulation of a gene comprising the nucleic acid molecule or	
CC	its encoded gene product. The method is used for diagnosing, preventing	
CC	or treating the disorder cited above, which may include Alzheimer's	
CC	disease, Parkinson's disease, depression, bipolar disorder.	
CC	schizophrenia, amnesia, headache, stroke, insomnia, alcohol abuse,	
CC	anxiety, chronic pain, retinal blastoma, primary retinal detachment or	
CC	age-related macular degeneration.	
XX		
XX	Sequence 2500 BP; 861 A; 431 C; 525 G; 683 T; 0 U; 0 Other;	

Query Match	7.3%;	Score 176.4;	DB 10;	Length 2500;
Best Local Similarity	49.6%;	Pred. No. 1.5e-28;		
Matches 617;	Conservative	0;	Mismatches 591;	Indels 36; Gaps 5;
QY	740	CAGACAACATACACTACTGGCTTATTGGCGACATCATATGTGATATCATCTACCTTTATG	799	
Db	605	CTGATTACCTAGATATTTGGCTCAATTTGGATTACGTATCAGACATAGTCTATTATTCG	664	
QY	800	ATATGCTATTATTCAGCCAGACTCCAGTTTGTAGAGGAGGAGACATAATAGTGGATT	859	
Db	665	ATATG---TTTGTACGAACAAGGACAGGTTACCTAGAAACAAGGACTCTCGTAAAGGAAG	721	
QY	860	CAAAATGAGCTAAGGAACACTACAGGACTTCTACAAAATTTTCAGTTGGATGTCGCATCAA	919	
Db	722	AACCTAAACCTCATATAATAATAATCCAACTTGCAAATTTAAACTTGTATGTTCTGTCC	781	
QY	920	TAATACCATTTGATATTTGCTACTCTCTCTTTGGGTTTA---ATCCAAATGTTTAGAGCAA	976	
Db	782	TGATACCAACTGATTTGCTGTATTTTAAAGTTAGGGTGGAACTATCCAGAAATTTAGATTAA	841	
QY	977	ATAGGATGTTAAAGTACACTTTCATTTTGTGAATTTAATCATCATCAGCTAGAGTCTATATGG	1036	
Db	842	ACAGGTTGTTACGGTTCTCTCGTATGTTTGAGTTCTTCCAGAGAACAGAAACAAGGACAA	901	
QY	1037	ACAAAGCATATATCTACAGAGTTATTTCGAACAACACTGGATACTTGTCTGTTATTCTGCACA	1096	
Db	902	ACTATCCAAACATCTTCAGGATTTCCAACTTGTATGTATATCGTCATCATTTATCCACT	961	
QY	1097	TTAATGCCCTGTGTTTATTACTGGGCTTCAAACCTATGAAGAAATGGGCATCTAGATGGG	1156	
Db	962	GGAAATGCATGTGTGTTCTACTCTATTCTTAAAGCTATTGGAATTTGGAATGATACATGGG	1021	
QY	1157	TGTA-----TGATGGGAAGGAACGAGTATCTGAGATGTT	1192	
Db	1022	TCTACCCCTGATATTAATGATTCCTGAATTTGGCCGTTTGGCTAGAAAATACGTATACAGCC	1081	
QY	1193	ATTATTGGGCAGGTTTCGAACTTTAAATTTACCAATTTGGTGGCTTCCAGAACCAACAACTTTAT	1252	
Db	1082	TTTACTGGTCTACACTGACTTTGACTTACCATTTGGTGAACACACCCCTCCCGTGAGGGATT	1141	
QY	1253	TTGAAATGTTTTTCAACTCTGAAATTTTTTTTCTGAGTTTTTGTGTTCTCCAGTTTAA	1312	
Db	1142	CTGAGTATGCTTTGTGGTGGTTGATTTCTCTAATTTGGAGTGTAAATTTTGTCTACCATCG	1201	
QY	1313	TTGGTCAGATGAGAGATGTGATTTGGAGCAGCTACAGCCAATCAGAACTACTTCCGCGCCT	1372	
Db	1202	TTGGTTACATAGGTTCTATGATTTCCAAATGAATGCAGCCAGCAGCAGCAATTTCAAGCAA	1261	
QY	1373	GCATGGATGACACCAATTCCTACATGAACAAATTTACTCCTTAAACTTTGTGCAAAAAGC	1432	
Db	1262	GAAATGATGCTATCAAGCAATATATGCAATTTTCCGAATGTAAAGCAAAAGATATGCAAGA	1321	
QY	1433	GAGTTTCGGAATTCGGTATGAATATACATGGGACTCTCAAGAGATGCTAGATGAGTCTGATT	1492	
Db	1322	GGGTTATTAAATGGTTTGTACTCTCTGGACCAACAAAAAACAAGTTGATGAGAAAAGAG	1381	
QY	1493	TGCTTAAAGCCCTACCAACTACGGTCCAGTTAGCCCTTCGCCCTTGTATGTGAACTTTCAGCA	1552	
Db	1382	TCITTAAAGTATCTACCTGATAAACTAAGAGCAGAAATTTGCCATCAACGTTTCACTTAGACA	1441	
QY	1553	TCATCAGCAAGTCGACTTGTTCAGGGTTGTGTATACACAGATGATTTTATGACATGTTGC	1612	
Db	1442	CATTAAAAAAGGTACGCAATTTTGTGCTGATTTGTGAAGCTGGTCTGTGTGGTGGATGTGTCT	1501	
QY	1613	TAAGATTGAAATCCGTTCTCTATTGTCCTGGTGACTTTGTCTGCAAAAAGGGAGAAATTCG	1672	
Db	1502	TGAATTTGCAACCCCAAGTCTACAGTCTCGAGATTATATTTTGCAGAAAAGGGGATATTCG	1561	
QY	1673	GCAGGAAATGTATATCATCAAGCATGGAGAGTCCAACTTCTTGGAGGCCCTGATGGTA	1732	
Db	1562	GACGAGAGATGTACATTATCAAGGAAGGCAAACTCGCTGTGTGGCAGATGATGGAGTCA	1621	





Db 1742 TGTTCCTCTCTCAAAAGATGACCTCATGGAAGCTCTAACTGAGTACCCAGATGCCAAA 1801  
QY 1907 GGATCCTCATGAAGAACCCAGAGTGTCTTTTAAAGCAGAGGCT 1950  
Db 1802 CTATGCTAGAGAAAAGGAAGCAAAATTTTAAATGAAAAGATGGT 1845  
RESULT 13  
AAS75291  
ID AAS75291 standard; cDNA; 289 BP.  
XX AC AAS75291;  
XX 13-FEB-2002 (first entry)  
XX DNA encoding novel human diagnostic protein #11095.  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX Homo sapiens.  
XX WO200175067-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US008631.  
XX 31-MAR-2000; 2000US-00540217.  
XX 23-AUG-2000; 2000US-00649167.  
XX (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
XX P-PSDB; ABG11104.  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX Claim 1; SEQ ID NO 11095; 103pp; English.  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
CC coding sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 289 BP; 105 A; 76 C; 57 G; 51 T; 0 U; 0 Other;  
Query Match 6.6%; Score 160.6; DB 5; Length 289;  
Best Local Similarity 86.0%; Pred. No. 2.3e-25;  
Matches 178; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 287 GAACAGTCCAGAGCAGAGAAATGGACCCCGGAAAGAGGTCCAAACAGCCCAAAA 346  
Db 83 GCAAACTATCACAAGGACAGAAAAACCAACAACCGCATGTTCTCACACAACAGCCCAAAA 142  
QY 347 ACAAAACCGCTCGAGCTCCTGTTTATAAATGAGTATGCGATGCCAGCTACACAACCTGG 406  
Db 143 ACAAAACCGCTCGAGCTCCTGTTTATAAATGAGTATGCGATGCCAGCTACACAACCTGG 202  
QY 407 TGAAGAAGATGCTCAAGAACAGCCCTCTACAGAAAAAGTTGGTAGAGGAGATCTCT 466  
Db 203 TGAAGAAGATGCTCAAGAACAGCCCTCTACAGAAAAAGTTGGTAGAGGAGATCTCT 262  
QY 467 CTTCAACCCGGAAGCCAGCCCAACAACTG 493  
Db 263 CTTCAACCCGGAAGCCAGCCCAACAACTG 289  
RESULT 14  
ABL18085  
ID ABL18085 standard; DNA; 2109 BP.  
XX ABL18085;  
XX 26-MAR-2002 (first entry)  
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 5728.  
XX Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical; gene; ds.  
XX Drosophila melanogaster.  
XX WO200171042-A2.  
XX 27-SEP-2001.  
XX 23-MAR-2001; 2001WO-US009231.  
XX 23-MAR-2000; 2000US-0191637P.  
XX 11-JUL-2000; 2000US-00614150.  
XX (PEKE ) PE CORP NY.  
XX Venter JC, Adams M, Li PWD, Myers EW;  
XX WPI; 2001-656860/75.  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signaling and cell-cell  
PT interactions.  
XX Claim 1; SEQ ID NO 5728; 21pp + Sequence Listing; English.  
XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 2109 BP; 485 A; 589 C; 605 G; 430 T; 0 U; 0 Other;  
Query Match 5.6%; Score 136.2; DB 4; Length 2109;  
Best Local Similarity 46.4%; Pred. No. 9.8e-20;  
Matches 607; Conservative 0; Mismatches 678; Indels 24; Gaps 4;  
QY 668 TCCTGTCACTCTTCGCTATATACTGAAGTGTGTTATACCACTGCGCTCTTCC 727



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Db 2 TGGTGGTGTCCATGGCCCTTCTGTACAACTTCTGGGTGATTAATCTACCGCTTCGGCTTCC 61
Qy 728 CATATCAAAACGCGACACATACACTACTGGCTTAATTCGGACATCATATGTGATATCA 787
Db 62 AGGAGATCAATCGGGCAACGATCGCAATTTGGTCTGTCTGACTACCTGTCCGACTTCC 121
Qy 788 TCTACCTTTATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTAGAGAGGAGACA 847
Db 122 TGTATCTGATCGATATACTGT---TCCACTTTCGCACCGGATACCTGGAGACGGGGTGC 178
Qy 848 TAATAGTGGATTCAAATGAGCTAAGGAAACACTACAGGACTTCTACAAAATTTTCAGTTGG 907
Db 179 TGCAGACGAGCGCTTGAAGCTGCGCACCCACTACATGAATCGACGATCTTCTACATCG 238
Qy 908 ATGTGCGCATCAATATACCAATTTGATATTTGCTACTCTTCTTTGGGTTTAAATCCAATGT 967
Db 239 ACTGCTGTGCTGTGCGCGTGGACTTTCTATTTGTCTCATCGGCTTTAACTCGATCC 298
Qy 968 TTAGAGCAATAGGATGTTAAAGTACACTTCAATTTTGGAAATTTAATCATCACCTAGAGT 1027
Db 299 TGCAGCGCTTCGGCTGGTGAAGATCTACCGGTTCTGGGCCCTTCATGGATCGCACCGAGC 358
Qy 1028 CTATAATGGACAAAGCATATATACAGAGTTATTCGAACAACTGGATCTGTGTTTA 1087
Db 359 GGCACACCACTACCCGNAACCTGTTCCGGAGCAGCGCCCTCATCTACTACTCTGTGTGA 418
Qy 1088 TTCTGCACATTAATGCCCTGTGTTTATTTACTGGGCTTCAAATCTATGAAGAAATTTGGCACTA 1147
Db 419 TATTCCATTGGAACGGTTGTCTTACCACATCATACACAAGAACAAATGGGTTCCGATCAC 478
Qy 1148 CTAGATGGGT-----GTATGATGGGGAAGAAACGAGTATCTGAGATGTT 1192
Db 479 GCAACTGGGTCTACCCAGACTCGGAGTCGGCGGACGTGGTCAAGCAGTATCTCGAGAGCT 538
Qy 1193 ATTATTGGCAGTTCGAACTTTAATTACCATTTGGTGGCTTCCAGAACCAAACTTTAT 1252
Db 539 ACTACTGGTGACCCCTGGCCCTGACCACCATCGGGGATCTTCCAAAGCCGCGTCCAAAG 598
Qy 1253 TTGAAATTTGTTTCAACTCTTGAATTTTCTGGAGTTTGTGTCTCCAGTTTAA 1312
Db 599 GCGAGTAGCTTTGTTATCTCGAGCTGCTTTTGGCTGATGCTCTTCGCCACGGTAC 658
Qy 1313 TTGCTCAGATGAGATGATGAGAGCTACAGCAATCAGCAACTACTTTCGCGCCT 1372
Db 659 TGGGCGCAGTGGCCAAACATTTGACGTCAGTGAGTCAGCGCGCAAGAGTTTCAAGCCA 718
Qy 1373 GCATGGATGACACCATTCCTTACATGACATTAATCTCCATTCCTAAACTTTCGCAAGC 1432
Db 719 AGCTGGATGGCGTGAAGACGTACATGCGGATGCGACGTTGTCGGAATCATCTCGAGGTGA 778
Qy 1433 GAGTTCCGACTTGGTATGAATATACATGGGACTCTCAAGAATGCTAGATGAGTCTGATT 1492
Db 779 AGGTCAATCAATGGTTGATTAACCTGTGGCTTACGCAAAATGCTCGACAGGAGCGC 838
Qy 1493 TGCTTAAGACCTTACCAATCAGGTCAGTTAGCCCTCGCCATGATGATGTAACCTTCAGCA 1552
Db 839 CCGTGTCTGCTCTCTGATATAATTAAGGCTGAATAGCAATTAACGTCATTTAGATA 898
Qy 1553 TCATCAGCAATGCTACTTGTTCAGGTTTGTGATACACATGATTTATACATGTTGC 1612
Db 899 CGCTCAAGCGGTGGAGATTTTCCAAAACACAGAGGCGCGCTTCTATGCGAATCTGGTGC 958
Qy 1613 TAAGATTAATTCGTTCTTATTTGCTGTGACTTTGTCTGCAAAAGGAGAAATTTG 1672
Db 959 TGCCTGTAGGCCCGTGTCTTCTGCGCCGCGACTACATCTGCAGAAAGGCGAGGTGG 1018
Qy 1673 GCAAGGAATGATATATCAAGCATGAGAGTCCAAAGTTCTTGGAGGCCCTGATGATA 1732
Db 1019 GCAAGGAGATGTACATTTGTAACGAGGACGATTCGAGTGTGGTGGCCGAC---AATGGAA 1075
Qy 1733 CTAAGTTCTGGTTACTCTGAAAGCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1792
Db 1076 AGACGGTATGGCCCTCCCTGGAAGGTGGTTCCTATTTTGGCGAGATTAGTATACTCAATA 1135
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Qy 1793 CAGG---AGGAGAAACCGTGAACCTGCCAACTGCCAATGTGGTGGCCACCGGTTTCCCAATCTTT 1849
Db 1136 TGGCACCGCAGGCAACCGACGACAGCCAGCGTTGCTCAGTGGGATACAGCGACCTCT 1195
Qy 1850 TAACTCTAGACAAAAGACCTCCAAAGAAATTTCTAGTGCATTTATCCAGATTTCTGNAAGGA 1909
Db 1196 TCGTCCCTGAGCAAGAAGACATGTGGGACGTGCTGAAAGAGTATCCGCGCGCGGTGTTTC 1255
Qy 1910 TCCTCATGAAGAAACCGACAGTGTCTTTTAAAGCAAGAGGCTTAAGACCGC 1958
Db 1256 GTCTGGAGTCGATAGCGTCAAGCGATTGGAGAAATACAGAAGGCCCC 1304
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## RESULT 15

ADF56505

ID ADF56505 standard; DNA; 3027 BP.

XX ADF56505;

XX DT 12-FEB-2004 (first entry)

XX DE Modified rat olfactory cyclic nucleotide-gated ion channel DNA #1.

XX KW ds; gene; olfactory cyclic nucleotide-gated ion channel;  
increased cAMP sensitivity; decreased cGMP sensitivity;  
decreased nitric oxide sensitivity;  
decreased calcium-calmodulin sensitivity.

XX OS Rattus norvegicus.

XX FH Key Location/Qualifiers  
FT CDS 340..2334  
/\*tag= a

XX FN US2003157571-A1.

XX PD 21-AUG-2003.

XX PF 15-NOV-2002; 2002US-00295573.

XX PR 16-NOV-2001; 2001US-0332494P.

XX XX (COLS ) UNIV COLORADO.

XX PI Karpen JW, Rich TC, Cooper DMF, Schaack J;

XX XX WPI; 2003-787336/74.

XX DR P-PSDB; ADF56501.

XX XX New nucleic acid encodes modified olfactory cyclic nucleotide-gated ion  
channels which exhibit increased sensitivity and specificity for cAMP and  
are useful to elucidate activities of proteins important in cAMP  
signaling.

XX PS Disclosure; SEQ ID NO 1; 63pp; English.

XX CC The invention relates to an isolated nucleic acid encoding a modified  
olfactory cyclic nucleotide-gated ion channel, where the channel  
comprises mutations which together impart increased cAMP sensitivity,  
decreased cGMP sensitivity, decreased nitric oxide sensitivity and  
decreased calcium-calmodulin sensitivity. The invention is used to  
elucidate activities of receptors, G-proteins, phosphodiesterases, adenylyl  
cyclases and other proteins important in cAMP signaling. The present  
sequence represents modified rat olfactory cyclic nucleotide-gated ion  
channel DNA.

XX SQ Sequence 3027 BP; 783 A; 698 C; 746 G; 800 T; 0 U; 0 Other;

Query Match

Best Local Similarity 5.5%; Score 133.2; DB 10; Length 3027;

Matches 623; Conservative 0; Mismatches 673; Indels 36; Gaps 5;



Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	2049.4	84.3	2135	4	US-09-949-016-1074	Sequence 1074, App
2	2035.4	83.8	2139	4	US-09-949-016-5798	Sequence 5798, App
3	330	13.6	99370	4	US-09-949-016-12816	Sequence 12816, App
4	330	13.6	99370	4	US-09-949-016-17540	Sequence 17540, App
C 5	329.6	13.6	601	4	US-09-949-016-38930	Sequence 38930, App
C 6	329.6	13.6	601	4	US-09-949-016-38931	Sequence 38931, App
C 7	329.6	13.6	601	4	US-09-949-016-205286	Sequence 205286, App
C 8	329.6	13.6	601	4	US-09-949-016-205287	Sequence 205287, App
C 9	202	8.3	601	4	US-09-949-016-38898	Sequence 38898, App
C 10	202	8.3	601	4	US-09-949-016-205176	Sequence 205176, App
11	181.2	7.5	2796	4	US-09-949-016-5678	Sequence 5678, App
12	169.8	7.0	84571	4	US-09-949-016-17420	Sequence 17420, App
C 13	151.4	6.2	601	4	US-09-949-016-38897	Sequence 38897, App
C 14	151.4	6.2	601	4	US-09-949-016-205175	Sequence 205175, App
C 15	147.6	6.1	601	4	US-09-949-016-38915	Sequence 38915, App
C 16	147.6	6.1	601	4	US-09-949-016-205232	Sequence 205232, App
C 17	144.6	6.0	601	4	US-09-949-016-205238	Sequence 205238, App
C 18	144.6	6.0	601	4	US-09-949-016-205229	Sequence 205229, App
C 19	143	5.9	601	4	US-09-949-016-38929	Sequence 38929, App
C 20	143	5.9	601	4	US-09-949-016-205285	Sequence 205285, App
C 21	132.8	5.5	3470	4	US-09-949-016-4344	Sequence 4344, App
C 22	132.8	5.5	32666	4	US-09-949-016-16086	Sequence 16086, App
C 23	102.6	4.2	601	4	US-09-949-016-38918	Sequence 38918, App
C 24	102.6	4.2	601	4	US-09-949-016-205235	Sequence 205235, App
C 25	93.8	3.9	7218	1	US-08-232-463-14	Sequence 14, App
C 26	91.4	3.8	601	4	US-09-949-016-38908	Sequence 38908, App
C 27	91.4	3.8	601	4	US-09-949-016-205201	Sequence 205201, App





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; Sequence 12816, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12816
; LENGTH: 99370
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-12816

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Query Match	13.8%;	Score 330;	DB 4;	Length 99370;
Best Local Similarity	100.0%;	Pred. No. 7e-74;		
Matches 330;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db				
Qy 96982	CAGAAGAAAGAAAATTTCTGAAGGAGAGAGAGGAAAGAGAAAAGAAAATGAAGATAAACAA	97041		
Db				
Qy 2161	AAAGAAAAATGAAGATATAACAAAAGAAAGAAAAATGAAGATAAAGGAAAAAGAAAATGAAGATAAA	2220		
Db				
Qy 97042	AAAGAAAAATGAAGATATAACAAAAGAAAGAAAAATGAAGATAAAGGAAAAAGAAAATGAAGATAAA	97101		
Db				
Qy 2221	GATAAAGGAAGAGAGCCAGAGAGAACCACTGGACAGACCTGGAATGTACAGCAAGTCCT	2280		
Db				
Qy 97102	GATAAAGGAAGAGAGCCAGAGAGAACCACTGGACAGACCTGGAATGTACAGCAAGTCCT	97161		
Db				
Qy 2281	ATTGCGAGTGGAGGAAGAACCCCACTCAGTTAGAAAGGACAGTTTTACCCAGAGGGACTTCT	2340		
Db				
Qy 97162	ATTGCGAGTGGAGGAAGAACCCCACTCAGTTAGAAAGGACAGTTTTACCCAGAGGGACTTCT	97221		
Db				
Qy 2341	CGTCAATCACTCAATTATCAGCATGGCTCCTTTCTGTGAGGGCGGAGAGAGGTTCTTACT	2400		
Db				
Qy 97222	CGTCAATCACTCAATTATCAGCATGGCTCCTTTCTGTGAGGGCGGAGAGAGGTTCTTACT	97281		
Db				
Qy 2401	ATTGGAAGTCAAGAAAGGCTTAAGCAATAA	2430		
Db				
Qy 97282	ATTGGAAGTCAAGAAAGGCTTAAGCAATAA	97311		
Db				

RESULT 4  
US-09-949-016-17540  
; Sequence 17540, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17540  
; LENGTH: 99370

[illegible]

RESULT 5  
US-09-949-016-38930/c  
Sequence 38930, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 38930  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-38930

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	Best Local Similarity	99.7%;	Pred. No. 6.6e-75;		
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Db	414	CAGAAGAAAGAAATTC	TGAAGGAGGAGAGGAAAGGAAATGAAGATAAACAA	355	
Qy	2161	AAAGAAATCGAAGATATAA	CAAAAAGAAATTAAGATAAAGGAAAGAAATGAAGATAAA	2220	
Db	354	AAAGAAATCGAAGATATAA	CAAAAAGAAATTAAGATAAAGGAAAGAAATGAAGATAAA	295	
Qy	2221	GATAAAGGAAGAGCGCAG	AGAAAGCCACTGGACAGACCTGTAATGTACAGCAAGTCCT	2280	
Db	294	GATAAAGGAAGAGCGCAG	AGAAAGCCACTGGACAGACCTGTAATGTACAGCAAGTCCT	235	







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Best Local Similarity	49.8%;	Prod. No. 2.6e-36;		
Matches 620;	Conservative	0;	Mismatches 586;	Indels 36; Gaps 5;
QY	740	CAGACAACATACACTACTCGCTTATTGGCGACATCATATGTATCATCTTACCTTTATG	799	
DB	897	CTGATTACCTGAATATTGGCTCATTTTGGATTACGTATCAGACATAGTCTATTTAATCG	956	
QY	800	ATATGCTATTTATCCAGCCAGACTCCAGTTTGTAAAGGAGGAGACATAATAGTGGATT	859	
DB	957	ATATG---TTTGTACGAACAGGACAGGTACCTAGAACAGGACTGCTGTAAGGAG	1013	
QY	860	CAAAATGAGCTAAGGAAACACTACAGGACTTCTACAAAATTTCAAGTTGGATCGCATCAA	919	
DB	1014	AACTTTAAACTATAAATAAATAAATCCAACTTGCAATTTAAACTTGATGCTTCTGTCCAC	1073	
QY	920	TAATACCACTTTGATATTGCTACCTCTCTTTGGGTTT---ATCCAAATGTTTGAAGCAA	976	
DB	1074	TGATACCAACTGATTGCTGTATTTTAAGTTAGGGTGGAACTATCCAGAAATTAGATTAA	1133	
QY	977	ATAGGATGTTAAAGTACACTTCATTTTGTGAATTTAAATCATCACTAGAGTCTATAATGG	1036	
DB	1134	ACAGGTTGTACGGTCTCTCGTATGTTTGAGTCTCCAGAGAACAGAAACAGGACAA	1193	
QY	1037	ACAAAGCATATATCTACAGAGTTATTCGAACAACATGGATACTTGTCTGTTATTCTGCACA	1096	
DB	1194	ACTATCCAAACATCTTCAGGATTTCCAACTTGTATGTATATCGTCATCATTTATCCACT	1253	
QY	1097	TTAATGCCCTGTGTTTATTACTGGGCTTCAAACATAGAAGGAATTTGGCNACTACTAGATGGG	1156	
DB	1254	GGAAATGCATGTGTGTTCTACTCTATTCTTAAAGCTATTGGAAATTTGGAAATGATCATGGG	1313	
QY	1157	TGTA-----TGATGGGGAAGGAAACGAGTATCTCGAGAGTGT	1192	
DB	1314	TCTACCTGTATTAATGAATCTGAATTTGGCCGTTTGGCTAGAAAATCGTATACAGCC	1373	
QY	1193	ATTATTGGCGAGTTCGAACCTTTAATTACATTTGGTGGCTTCCAGAACCAAAACTTTAT	1252	
DB	1374	TTTACTGTGCTACACTGACTTTGACTACCATTTGTGAAACACCCCTCCCGTGAGGGATT	1433	
QY	1253	TTGAAATTTGTTTTTCAACTCTTGAAATTTTTTTCTGGAGTTTTTGTGTTCTCCAGTTTAA	1312	
DB	1434	CTGAGTATGTCTTTGTGGTGTGATTTTCTTAATTGGAGTGTTAATTTTGTCTACCATCG	1493	
QY	1313	TTGGTCAGATGAGAGATCTGATTTGGAGCAGCTACAGCCAATCAGAACTACTTCCGCGCT	1372	
DB	1494	TTGGTAAATAGTTTCTATGATTTTCCAAATGAATGCAGCAGACAGAAATTTCAAGCAA	1553	
QY	1373	GCATGGATGACACCAATTGCCTACATGAACAAATTACTCCATTCTTAAACTGTGCAAAAGC	1432	
DB	1554	GAAATTGCTATCAAGCAATATATGCAATTTTCGNAATGTAAAGCAAGATATGGAAGA	1613	
QY	1433	GAGTTCCGACTTGGPATGAATATACATGGGACTCTCAAAGAAATGCTAGATGAGTCTGATT	1492	
DB	1614	GGGTTATTTAAATGGTTTGTACTACCTGTGGAACCAACAAATAACAGTTTGTAGAGAAAGA	1673	
QY	1493	TGCTTTAAGACCCTACCACTACGGTCCAGTTTAGCCCTCGCCATTTGATGTGNACTTCAGCA	1552	
DB	1674	TCTTAAAGTATCTACCTCGATAAATTAAGAGCAGAAATTTGCCCATCAACGTTTCACTTAGACA	1733	
QY	1553	TCATCAGCAAGTCGACTTGTTCAGGGTCTGTATACACATGATTTATGACATGTTTC	1612	
DB	1734	CATTAAAAAGGTACCGCAATTTTGTGTAATGTGTAAGCTGGTCTGTTGGTGGAGTTGGTCT	1793	
QY	1613	TAAGATTGAAATCCGTTCTCTATTGTCCTGGTGTACTTTGTCTGCAAAAAGGGAGAAATTG	1672	
DB	1794	TGAAATTGCAACCCCAAGCTACAGTCTCTGGAGATTATTTTTCAGAAAGGGGATATCG	1853	
QY	1673	GCAAGGAAATGTATATCATCAAGCATGGAAGTCCAAAGTTCTTTGGAGGCCCTGATCGTA	1732	
DB	1854	GACGAGAGATGTACATTTATCAAGGAAGGCAAACTCGCTGTGGTGGCAGATGATGGAATCA	1913	

RESULT 12

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US-09-949-016-17420
; Sequence 17420, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17420
; LENGTH: 84571
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(84571)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17420

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Query Match	7.0%;	Score 169.8;	DB 4;	Length 84571;
Best Local Similarity	49.6%;	Pred. No. 1.3e-32;		
Matches 571; Conservative	0;	Mismatches 547;	Indels 33;	Gaps 4;
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Dd	80762	TAGAACAAGGACCTCGTGTTAAGGAAGAACCTTAAACTCATAAATATAATCAAACCT	80821	
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Qy	893	CAAAAATTTTCAGTTGGATGTCGCCATCAATAATACCATTTCGATTATTTGCTACCTCTTCTTTTG	952	
Dd	80822	TGCAATTTAAACTGTGTTCTGTCTGCTACGATACCACTGATTTGCTGTATTTTAAGTTAG	80881	
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Qy	953	GGTTTTA---ATCCAAATGTTTAGAGCAAAATAGGATGTTAAAGTACACTTCATTTTTTGAAT	1009	
Dd	80882	GGTGGAACTATCCAGAAATTAGATTAAACAAGGTTGTACGGTTCTCTCGTATGTTTGAGT	80941	
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Qy	1010	TTAATCATCACCTAGAGTCTATATGAGCAAAAGCATATATCTACAGAGTTATTCCGAACNA	1069	
Dd	80942	TCMTCCAGAAACAGAAACAAGGCAAACTATCCAAACATCTTCAGGATTTTCCAACCTTG	81001	
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Qy	1070	CTGGATACCTTGCTGTTTATTCTGCACATTTAATGCGTGTGTTTATTACTGGGCTTCCAAACT	1129	
Dd	81002	TTATGTTATATCGTCATCATTTATCCACTGGAAATGCAATGTGTGTTCTACTCTATTTCTAAAG	81061	
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Qy	1130	ATGAAGGAATTGGCACTACTAGATGGGTGTA-----TGATG	1165	
<hr/>				
Dd	81062	CTATTGGATTTGGAAATGATACATGGGTCTACCCCTGATTTAAATGATCCTGAAATTTGGCC	81121	

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QY 1166 GGAAGGAAACGAGTATCTGAGATGTTATTATTGGCAGGTTGAACTCTTAATTAACCATTC 1225
Db 81122 GTTTGGCTAGAAATAGTATACAGCCCTTTACTGGTCTACACTGACTTTGACTACCATTCG 81181
QY 1226 GTGGCCCTCCAGAACCAAACTTTTAFTTGAATTTGTTTTCAACTCTTGAATTTTTTTT 1285
Db 81182 GTGAACACCCCTCCGCTGAGGATTCAGATATGCTTTGTGGTGGTTGATTTCCTAA 81241
QY 1286 CTGGAGTTTGTGTTCTCAGTTTAAATTTGGTCAGATGAGAGATGTGATTTGGAGCAGCTA 1345
Db 81242 TTGGAGTGTAAATTTTGTCTACCATCGTTGGTAAACATAGTCTTATGATTTTCCAACATGA 81301
QY 1346 CAGCCATCAGAACTACTTCGCGCCCTGCACTGATGATGACACCATTTGCTCATCAACAAT 1405
Db 81302 ATGACGACGAGCAGAAATTTCAAGCAAGAAATGATGCTATCAAGCAATATATGCAATTTTC 81361
QY 1406 ACTCCATTCCTAACTTTGTGCAAAAGCGAGTTCCGACTTGGTATGAATATACATGGGACT 1465
Db 81362 GAAATGTAAGCAAGATATGAAAAGAGGGTTATTAATGGTTTGACTACCTGTGGACCA 81421
QY 1466 CTCAAGAAATGCTAGATGATCTGATTTGCTTAAGACCCCTACCACTACGGTCCAGTTAG 1525
Db 81422 ACAAAAAAAGCAGTTGATGAGAAAGAGTCTTAAAGTATCTACCTGATAAATAAGAGCAG 81481
QY 1526 CCCTCGCCATTGATGTGAACCTTCAGCATCATCAGCAAGTCGACTTGTTCAGGGTTGTG 1585
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Db 81542 AAGCTGCTGTTGGTGGAGTTGCTTGAATTTGCAACCCCAAGTCTACAGTCCCTGGAG 81601
QY 1646 ACTTGTCTGCAAAAGGGAGAAATTTGGCAAGAAATGATATATCATCAAGCATGGAGAAG 1705
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QY 1706 TCCAAGTCTTGGAGGCCCTGATGTACTAAAGTCTCTGTT---TACTCTGAAAGCTGGG 1761
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Db 81722 TCGGTGAGATCAGCAATCTTAAATTAAGGGAGCAAGCTGCAATCGAAGAACGCCA 81781
QY 1820 ATGTGTGGCCCAAGGGTTGGCAATCTTTTAACTCTAGACAAAAAGACCCCTCCAAGAA 1879
Db 81782 ATATTAAGATATTGGCTACTCAGACCTGTTCTCTCTCAAAAGATGACCTCATGGAAG 81841
QY 1880 TTCTAGTGCAATATCCAGATTTCTGAAAGGATCTCATGAAGAACCCAGATGCTTTTAA 1939
Db 81842 CTCTAACTAGTACCCAGATGCCAAACTATGCTGGAAGAGAAAGGGAAGCAGATTTTAA 81901
QY 1940 AGCAGAAGGCT 1950
Db 81902 TGAAGATGCT 81912
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## RESULT 13

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US-09-949-016-38897/c
; Sequence 38897, Application US/09949016
; Patent No. 6812339
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## GENERAL INFORMATION:

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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastsEQ for Windows Version 4.0
; SEQ ID NO 38897
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-38897
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Query Match 6.2%; Score 151.4; DB 4; Length 601;
Best Local Similarity 99.3%; Pred. No. 5.8e-29;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 291 GCAAGCCACCGCTGTACCAAGTAAAGAAAGCGATGAAGCCACAGAACATTAC 232
QY 553 TACAGGCTGTTGTTGTTCAAAAGTCAAAAAGATGCCCTTTAAACAGAGTACTTTAAAGCGAAAT 612
Db 231 TACAGGCTGTTGTTGTTCAAAAGTCAAAAAGATGCCCTTTAAACAGAGTACTTTAAAGCGAAAT 172
QY 613 AAACCTTCCAAAACAGCATAGATTCATACACAGAT 645
Db 171 AAACCTTCCAAAACAGCATAGATTCATACACAGGT 139
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## RESULT 14

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US-09-949-016-205175/c
; Sequence 205175, Application US/09949016
; Patent No. 6812339
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## GENERAL INFORMATION:

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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastsEQ for Windows Version 4.0
; SEQ ID NO 205175
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-205175
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Query Match 6.2%; Score 151.4; DB 4; Length 601;
Best Local Similarity 99.3%; Pred. No. 5.8e-29;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 493 GCAAGCCACCGCTGTACCAAGTAAAGAAAGCGATGAAGCCACAGAACATTAC 552
Db 291 GCAAGCCACCGCTGTACCAAGTAAAGAAAGCGATGAAGCCACAGAACATTAC 232
QY 553 TACAGGCTGTTGTTGTTCAAAAGTCAAAAAGATGCCCTTTAAACAGAGTACTTTAAAGCGAAAT 612
Db 231 TACAGGCTGTTGTTGTTCAAAAGTCAAAAAGATGCCCTTTAAACAGAGTACTTTAAAGCGAAAT 172
QY 613 AAACCTTCCAAAACAGCATAGATTCATACACAGAT 645
Db 171 AAACCTTCCAAAACAGCATAGATTCATACACAGGT 139
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## RESULT 15

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US-09-949-016-38915/c
; Sequence 38915, Application US/09949016
; Patent No. 6812339
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; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 38915  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-38915

Query Match 6.1%; Score 147.6; DB 4; Length 601;  
Best Local Similarity 97.4%; Pred. No. 5.5e-28;  
Matches 150; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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Db 601 GGAGCAGCTACAGCCAATCAGAACTACTTCCGCGCCTGCATGGATGACACCAATTGCCTAC 542  
Qy 1396 ATGAACAATTACTCCATTCCTAACTTGTGCAAAAGCGAGTTCGGACTTGGTATGAATAT 1455  
Db 541 ATGAACAATTACTCCATTCCTAACTTGTGCAAAAGCGAGTTCGGACTTGGTATGAATAT 482  
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Db 481 ACATGGGACTCTCAAAGAAATGCTAGATGAGTCTG 448

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Perfect score: 2430  
Sequence: 1 atgtttaatcgctgacaaa.....aagaaaggctaagcaataa 2430

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 11104416

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2430	100.0	2657	11	US-09-855-828-16
4	577.4	23.8	4382	17	US-10-189-507-3
5	577.4	23.8	4382	17	US-10-159-563-147
6	306	12.6	680	13	US-10-027-632-204539
7	306	12.6	680	17	US-10-027-632-204539
8	176.4	7.3	2500	17	US-10-172-118-427
9	176.4	7.3	2500	17	US-10-342-887-427
10	133.2	5.5	3027	16	US-10-295-573-1
11	132.8	5.5	2085	15	US-10-345-680-27
					Sequence 3, Appli
					Sequence 2, Appli
					Sequence 16, Appli
					Sequence 3, Appli
					Sequence 147, App
					Sequence 204539,
					Sequence 427, App
					Sequence 1, Appli
					Sequence 27, Appli

12	132.8	5.5	3486	15	US-10-345-680-25	Sequence 25, Appli
13	131.6	5.4	1995	15	US-10-087-217-1	Sequence 1, Appli
14	131.6	5.4	1995	15	US-10-087-217-5	Sequence 5, Appli
15	131.6	5.4	3027	16	US-10-295-573-2	Sequence 2, Appli
16	131.6	5.4	3027	16	US-10-295-573-4	Sequence 4, Appli
17	129	5.3	526	9	US-09-864-761-12975	Sequence 12975, A
18	128.4	5.3	1995	15	US-10-087-217-3	Sequence 3, Appli
19	128.4	5.3	1995	15	US-10-087-217-7	Sequence 7, Appli
20	128	5.3	2877	16	US-10-295-573-3	Sequence 3, Appli
21	127	5.2	127	9	US-09-864-761-29538	Sequence 29538, A
22	111.2	4.6	1995	9	US-09-735-927-1	Sequence 1, Appli
23	111.2	4.6	1995	13	US-10-034-843-1	Sequence 1, Appli
24	111.2	4.6	1995	16	US-10-168-651-34	Sequence 34, Appli
25	111.2	4.6	1995	17	US-10-189-507-1	Sequence 1, Appli
26	111.2	4.6	2111	16	US-10-114-153-17	Sequence 17, Appli
27	111.2	4.6	2190	14	US-10-029-677-23	Sequence 23, Appli
28	111.2	4.6	12017	9	US-09-735-927-3	Sequence 3, Appli
29	109.6	4.5	1995	17	US-10-189-507-4	Sequence 4, Appli
30	109.6	4.5	2186	14	US-10-029-677-1	Sequence 1, Appli
C	84	3.5	31124	13	US-10-087-192-463	Sequence 463, App
32	83	3.4	472	18	US-10-674-124A-5858	Sequence 5858, Ap
33	82.6	3.4	336	18	US-10-674-124A-14888	Sequence 14888, A
34	81	3.3	625	13	US-10-027-632-179350	Sequence 179350,
36	80	3.3	2232	14	US-10-087-464-45	Sequence 179350,
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C	79.6	3.3	305	9	US-09-864-761-19262	Sequence 19262, A
C	79.6	3.3	496	9	US-09-864-761-2534	Sequence 2534, Ap
C	79.2	3.3	37265	13	US-10-087-192-49	Sequence 49, Appli
C	79.2	3.3	39443	17	US-10-085-117-313	Sequence 313, App
C	79	3.3	276	9	US-09-864-761-20595	Sequence 20595, A
C	79	3.3	462	9	US-09-864-761-3829	Sequence 3829, Ap
C	79	3.3	1728	9	US-09-927-267-3	Sequence 3, Appli
45	79	3.3	1728	17	US-10-189-507-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-855-828-3  
; Sequence 3, Application US/09855828  
; Publication No. US20040137433A1  
; GENERAL INFORMATION:  
; APPLICANT: Cresch, Christopher D.  
; APPLICANT: Jegla, Timothy J.  
; APPLICANT: ICAGEN, Inc.  
; TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel  
; FILE REFERENCE: 018512-006010US  
; CURRENT APPLICATION NUMBER: US/09/855,828  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: US 60/204,445  
; PRIOR FILING DATE: 2000-05-15  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 2430  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human CNG3B coding sequence  
; NAME/KEY: CDS  
; LOCATION: (1)..(2430)  
; OTHER INFORMATION: CNG3B  
US-09-855-828-3

Query Match 100.0%; Score 2430; DB 11; Length 2430;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGTTTAATCGCTGACAAAGTCAACAGGTGAAGCCTATAGAGAGAAACAATGAGAAAT 60  
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Db 1 ATGTTTAAATCGCTGACAAAAAGTCAACAAGGTGAAGCCTATAGGAGAGAAACAATGAAAT 60  
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Qy 901 CAGTTGGATGCGCATCAATAATCAATTTGATATTTGCTACCTCTCTTTGGGTTAAT 960  
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Db 1141 GGCACCTACTAGATGGGTGATGATGGGAAGGAAACGAGTATCTGAGATGTTATTATTGG 1200  
Qy 1201 GCAGTTTCGAACCTTTAATTAACCATTTGGTGGCTTCCAGAACCAAACTTTATTGAAAT 1260  
Db 1201 GCAGTTTCGAACCTTTAATTAACCATTTGGTGGCTTCCAGAACCAAACTTTATTGAAAT 1260  
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Qy 1921 AAAGCCAGAGTCTTTTAAAGCAGAGGCTAAGACCGCAGAGAACCAACCCCTCCAGAAAA 1980  
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QY 1981 GATCTTGGCCCTCTCTTCCACCGAAGAGAGACACCCAAACTGTTTAAAACTTCTCTTA 2040
Db 2043 GATCTTGGCCCTCTCTTCCACCGAAGAGAGACACCCAAACTGTTTAAAACTTCTCTTA 2102
QY 2041 GGAGGCACAGGAAAGCAAGTCTTGCAAGACTACTCAATTTGAAGCGAGAGCAAGCAGCT 2100
Db 2103 GGAGGCACAGGAAAGCAAGTCTTGCAAGACTACTCAATTTGAAGCGAGAGCAAGCAGCT 2162
QY 2101 CAGAGAAAGAAATTTCTGAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
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QY 2161 AAAGAAATGAAGATAAAACAAAAGAGAAATGAAGATAAAAGAGAAAGAGAAATGAAGATAAA 2220
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RESULT 3  
US-09-855-828-16  
; Sequence 16, Application US/09855828  
; Publication No. US20040137433A1  
; GENERAL INFORMATION:

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; APPLICANT: Creech, Christopher D.  
; APPLICANT: Jegla, Timothy J.  
; APPLICANT: ICagen, Inc.  
; TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel  
; FILE REFERENCE: 018512-006010US  
; CURRENT APPLICATION NUMBER: US/09/855,828  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: US 60/204,445  
; PRIOR FILING DATE: 2000-05-15  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 2757  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: complete CNG3B sequence derived from assembly of  
; OTHER INFORMATION: PCR fragments  
; NAME/KEY: CDS  
; LOCATION: (112)..(2541)  
; OTHER INFORMATION: CNG3B  
US-09-855-828-16
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Query Match 100.0%; Score 2430; DB 11; Length 2757;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 ACAGCACAGGAAGAAAACAAAGGTGAAGAGAAATCTCTCAAAAACCAAGTCAACTCCAGTC 180
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QY 181 AGTCTGAAGAGCCACACCAACATACAAAGTCAAGTCAAACTCTCCAGAAAATTCCTCTGGA 240
Db 292 AGTCTGAAGAGCCACACCAACATACAAAGTCAAGTCAAACTCTCCAGAAAATTCCTCTGGA 351
QY 241 GATCTGACCAAAACCCCTGACCCCTCAAAATGAGAGAGAACTCAAGTGAAGTCCAGAG 300
Db 352 GATCTGACCAAAACCCCTGACCCCTCAAAATGAGAGAGAACTCAAGTGAAGTCCAGAG 411
QY 301 CAGAGGAAATCGACCCCGGGAAGAGGTCAAAACAGCCCAAAAACCAAAACCGCCCTGCA 360
Db 412 CAGAGGAAATCGACCCCGGGAAGAGGTCAAAACAGCCCAAAAACCGCCCTGCA 471
QY 361 GCTCTGTTTATAATGAGTATGCCGATGCCAGTCTACAACTGGTGAAGAAAGTCCGT 420
Db 472 GCTCTGTTTATAATGAGTATGCCGATGCCAGTCTACAACTGGTGAAGAAAGTCCGT 531
QY 421 CAAAGAACAGCCCTCTTACAAAGAAAAGTTGGTAGAGGAGATCTCTCTCACCCGAAGCC 480
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QY 481 AGCCCAAAAATGCAAAAGCCCAAGGTGTACCAAGTAAAGAAAGCAAGCATGATTAAGCCA 540
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QY 541 ACAGAACATTAAGTACAGGCTGTTGGTTCAAAGTCAAAAGATGCTTTTACAGAGTAC 600
Db 652 ACAGAACATTAAGTACAGGCTGTTGGTTCAAAGTCAAAAGATGCTTTTACAGAGTAC 711
QY 601 TTAAAGCGAAATTAAGTCTTCAAAACAGCATAGATTTCATACACAGATCGACTTATCTCTG 660
Db 712 TTAAAGCGAAATTAAGTCTTCAAAACAGCATAGATTTCATACACAGATCGACTTATCTCTG 771
QY 661 TGGCTCTTGTGTCACACTCTTGCCTATATAACTGGAAGTCTGCTGTTTATACCACTGCGCCTC 720
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Db	1852	CTGTTTACTCTGAAGCGTCGGTCGGTGTTTGGAGAATAACGCCCTTCTAGCAGCAGGAGGA	1911
Qy	1801	GGAACCCGTGAACTGCCAATGTGGTGGCCACCAGGGTTTGCCCAATCTTTTAACCTCTAGAC	1860
Db	1912	GGAACCCGTGAACTGCCAATGTGGTGGCCACCAGGGTTTGCCCAATCTTTTAACCTCTAGAC	1971
Qy	1861	AAAAAGACCCTCCAGANAATTCTAGTGCAATTATCCAGATTCTGNAAGGATCCTCTGAAG	1920
Db	1972	AAAAAGACCCTCCAGANAATTCTAGTGCAATTATCCAGATTCTGNAAGGATCCTCATGAAG	2031
Qy	1921	AAAGCCAGAGTGTCTTTTAAAGCAGAAGGCTTAAGACCGCAGAAGCAACCCCCTCCAAGAAAA	1980
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Qy	2041	GGAGGCACAGAAAAGCAAGTCTTGCAGACTACTCAAATTTGAAGCGAGAGCAAGCAGCT	2100
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Qy	2221	GATAAAGGAAGAGAGCCAGAAGAAAGCCACTGGACAGACCTCAATGTATCAGCAAGTCCT	2280
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Qy	2281	ATTGCGAGTGGAGAAAGAACCCCACTCAGTTTAGAGACAGTTTTTACCCGAGGGACTTCT	2340
Db	2392	ATTGCGAGTGGAGAAAGAACCCCACTCAGTTTAGAGACAGTTTTTACCCGAGGGACTTCT	2451
Qy	2341	CGTCAATCACTCAATATCAGCATGGCTCTTCTGCTGAGGGCGGAGAAAGGTTCTTACT	2400
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Qy	2401	ATTGAAGTCAAGAAAAGGCTTAAGCAATAA	2430
Db	2512	ATTGAAGTCAAGAAAAGGCTTAAGCAATAA	2541

## RESULT 4

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US-101-189-507-3
; Sequence 3, Application US/10189507
; Publication No. US2003028633A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
; APPLICANT: XU, HONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: MOYER, BRYAN
; APPLICANT: PROMIN, ALEXEY
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: SERVANT, GUY
; APPLICANT: CALLAMARAS, NICHOLAS
; TITLE OF INVENTION: EXPRESSION OF
; TITLE OF INVENTION: NUCLEOTIDE GASE
; TITLE OF INVENTION: CELLS AND USE
; TITLE OF INVENTION: SNELL MODULAT
; FILE REFERENCE: 078003-0291567
; CURRENT APPLICATION NUMBER: US/10/
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: 60/303, 1
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/337, 1
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ IDS NOS: 12
; SOFTWARE: PatenIn Ver. 2.1

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; SEQ ID NO 3
; LENGTH: 2607
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-189-507-3

Query Match      23.8%; Score 577.4; DB 17; Length 2607;
Best Local Similarity 64.3%; Pred. No. 2.1e-114;
Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;

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QY      677  CTCCTTGCTATAACTCGAACTGCTGGTTTATACCACCTCGCGCTCGTCTTCCCATATCAA 736
DB      842  TGATGGCTGGAATTGGAATGTTGGCTGATCCCGTGGCTGGCCCTTCCCTTACCAGA 901

QY      737  CCGCAGACACATACATCTACTGGCTTATTCGGGCATCATATGATGATATCATCTACTTT 796
DB      902  CCCCGACAAATCCACCACTGGCTGCTGATGGATTACCTATGCGAAGCTCATCTACTTCC 961

QY      797  ATGATATGCTATTATCCAGCCAGACTCCAGTTTGTAAAGGAGGAGACATATAGTGG 856
DB      962  TGGACATCACCGTGTCCAGACAGCCTGCAGTTTGTCCAGAGGGGGGACATCATACGG 1021

QY      857  ATTCAATGAGCTAAGGAAACACTACAGGACTTCTACAAATTTTCAGTTGGATGTCGAT 916
DB      1022  ACAAAAGGACATCGGAATAATCTACTGTAAGTCTCCCGCTTCAAGATGGACCTGTCTCA 1081

QY      917  CAATAATPACATTTGATATTGTGTACCTCTCTTTTGGGTTTAAATCCAAATGTTTAGACAA 976
DB      1082  GCCTCTGCTCTTTGATTTTCTCTATTGAAAGTCGGTGTGAACCCCTCTCTCGCGCTGC 1141

QY      977  ATAGGATGTTAAAGTACACTTTTGTGAAATTAATCATCACTAGAGTCTATATAGG 1036
DB      1142  CCGCTGTGTTAAAGTACATGCGCTTCTTCAGATTTTAAACGCGCTGGAATCCATCTCA 1201

QY      1037  ACAAGGATATATCTACAGAGTTATTTCGAAACAATCTGATATCTGCTTTTATCTGCACA 1096
DB      1202  GAAAGCTACGTGTACAGGTCTATCAGHACCAAGCTTCTCTCTACAGCTGTGATT 1261

QY      1097  TTAATGCTGTGTTTATTACTTGGGCTTTCAAATATGAAGGAATTTGGCACTACTAGATGG 1156
DB      1262  TGAATTCCTGCTTTTATTACTTGGGCTCGGCTATCAGGCGCTCGGCTCACTCACTGGG 1321

QY      1157  TGTATGATGGGGAAGGAAACAGATATCTGAGATGTTATATTTGGGCAAGTTTCAACTTAA 1216
DB      1322  TTTACGATGCGTGGGAAACAGTTATATCGCTGTTACTATTTTGTGTGAAGACCTCA 1381

QY      1217  TTACCAATGTGTGCTTCCAGAACCAAACTTTTATTTGAAATTTGTTTTCAACTTTGA 1276
DB      1382  TCACCATCGGGGGCTCGCTGACCCCAAGACACTCTTTTGAATTTGTTTCCAGCTGTGA 1441

QY      1277  ATTTTATTTTCTGGAGTTTGTGTTCTTCCAGTTTAAATTTGTTTCAGATGAGAGATGTGATTG 1336
DB      1442  ATTTATTTTACGGGCGTCTTTGCTTTCTCTGTGATCGGACAGATGAGAGATGTGTGTAG 1501

QY      1337  GAGAGCTACAGCCAATCAGAACTACTTTCGGCGCTCGATGATGATGACCAATTTCCCTTACA 1396
DB      1502  GGGCGGCGCACCGGGGACAGACCTTACTTACCGCAGCTTCATGGACAGCACGCTGAAGTACA 1561

QY      1397  TGACCAATTAATCTCAATTCCTTAACTTTGTGCAAAAGCGAGTTTCGGACTTGTGTGAATATA 1456
DB      1562  TGAATTTCTACAAGATCCCCAAGTCCGTGCGAAGACCGCGCTCAAGACTGTGTACGAGTACA 1621

QY      1457  CATGGGACTCTCAAAGAATGCTAGATCAGTCTGATTTTGTCTTAAGACCCCTTACCACCTACGG 1516
DB      1622  CCTGGCACTCGAAGGCAATGCTGGATGAGTCAGAGCTGATGGTGCAGCTTCCAGACAGA 1681

QY      1517  TCCAGTTAGCCCTCGCCATTTGATGTGAATCTTACGATCATCAGCAAAAGTCACTGTGTTC 1576
DB      1682  TGGCGGTGGAACCTCGCCATCGAAGTAACTTACAACTCGTTAGCAAAAGTGCACCTCTTTC 1741

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Qy	1577	AGGTTGTGTATGACACAGATGATTTATGACATGTTGCTAAGATTGAAATCCGTTCTCTATT	1636
Db	1742	AGGGCTGTGACCGGCAGATGATCTTTTGACATGCTGAAGAGGCTTCGGCTCTGTTGTCTTACC	1801
Qy	1637	TGCTGTGTGACTTTGTCTGCAAAAGGGAGAAATTGCGAAGGAAATGTATATCATCAAGC	1696
Db	1802	TGCCCAACGACTATGTGTGCAAGAAGGGGAGATCGGCCGTGAGATGTATCATCATCCAGG	1861
Qy	1697	ATGGAAGTCCAAAGTTCTTTGGAGGCCCTGATCGTACTAAAGTCTTGGTTTACTCTGAAAG	1756
Db	1862	CAGGCAAGTGCAGGTTCTTGGCGCGCCCTGATCGGAAATCTGTGCTGGTGACGCTGAAG	1921
Qy	1757	CTGGGTCGGTGTTTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGAGAAACCGTCGAACTG	1816
Db	1922	CTGGATCTGTGTTTGGAGAAATAAGCTTGTGCTGTGTGGGGCGGAAACCGGCGCACGG	1981
Qy	1817	CCAAATGTGTGGCGCACGGGTTTGGCAATCTTTTAATCTAGACAAAAAGACCCCTCAAG	1876
Db	1982	CCAAACGTGTGGCGCACGGGTTTACCAACTCTTCATCTCGTGGATAAGAAGGACCTGAAATG	2041
Qy	1877	AAATCTTAGTGCAATATCCAGATCTCTGAAGGATCTCATGAAGAAAGCCAGAGTGTCTTT	1936
Db	2042	AGATTTTGGTGCATATCTCTGAGTCTCAGAAGTTACTCCGGAAGAAAGCCAGGCGCATGC	2101
Qy	1937	TAAAGCAGAAGGCTTAAGACCGCAGAAG	1963
Db	2102	TGAGAGCAACATAAGCCCAAGAGG	2128
RESULT 5			
US-10-159-563-147			
; Sequence 147, Application US/10159563			
; Publication No. US20040009154A1			
; GENERAL INFORMATION:			
; APPLICANT: Khan, Javed			
; APPLICANT: Ringner, Markus			
; APPLICANT: Peterson, Carsten			
; APPLICANT: Meltzer, Paul			
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR			
; ; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCER			
; FILE REFERENCE: 11613.56U511			
; CURRENT APPLICATION NUMBER: US/10/159,563			
; CURRENT FILING DATE: 2002-12-09			
; PRIOR APPLICATION NUMBER: US 10/133,937			
; PRIOR FILING DATE: 2002-04-25			
; NUMBER OF SEQ ID NOS: 444			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 147			
; LENGTH: 4382			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-159-563-147			

	Query Match	23.8%	Score 577.4	DB 17	Length 4382	
	Best Local Similarity	64.3%	Pred. No. 2.6e-114			
	Matches 866	Conservative 0	Mismatches 481	Indels 0	Gaps 0	
Qy	617	TTCCAAACAGCATAGATTCAATACACAGATCGACTCTATCTCTGTGGCTCTTGCTGTGCA	676			
Db	1983	TTTCCCAGAGCATTTGACCCGCTGACCAACTGATGATGTCCTATGCTTCTTTCGTGG	2042			
Qy	677	CTCTTGCGCTATACCTGGAACTGCTGGTTTATACCACTGGCGCTCGTCTTCCCATATCAAA	736			
Db	2043	TGATGGCTCGGAATTGGAACTGTTGGCTGANTCCCGTGGCTGGGGCTTCCCCCTACCAGA	2102			
Qy	737	CCGCAGACAAACATACACTACTGCTCTTATTGCGACATCATATGTGATATCATCTACTCTTT	796			
Db	2103	CCCGGACACATCCACCACTGGCTGCTGATGATTAACCTATGCGACCTCATCTACTTCC	2162			
Qy	797	ATGATATGCTATTATTATCCAGCCACAGACTCCAGTTTCTTAAGAGGAGAGACATTAATAGTGG	856			
Db	2163	TGGACATCACCGTGTGTTCCAGACACGCGCTGCAGTTTCTCAGAGCGGGGACATCATTTACGG	2222			

QY 857 ATTCAATGAGCTAAGAAACACACTACGAGCTTCTCAAAAAATTTTCAGTTGGATGTCGAT 916  
Db 2223 ACAAAGGACATGCGAAATAACTACCTGAAGTCTCGCGCTTCAAGATGACCTGCTCA 2282  
QY 917 CAATAATACCAATTTGATATTGCTACCTCTCTTTGGGTTTAATCCAAATGTTTAGAGCA 976  
Db 2283 GCCTCTGCCCTTGATTTCTCTATTTGAAAGTCGGTGTGAACCCCTCTCCGCCCTGC 2342  
QY 977 ATAGATGTTAAAGTACACTCTTATTTTGTGAATTAATCATCACCTAGAGTCTATAATGG 1036  
Db 2343 CCGCTGTTTAAAGTACATGCGCTTCTCGAGTTTAAAGCGCGCTGAAATCCATCTCA 2402  
QY 1037 ACAAAGCATATCTACAGAGTTATTCGAACAACTGAGTACTTGTCTTTTATTTCTGCACA 1096  
Db 2403 GCAAAGCCTAGCTGTACAGGGTCAACAGCCACAGCCTACCTTCTTACAGCCTGCATT 2462  
QY 1097 TTAATGCTGTTTATTTACTGGGCTTCAAACTATGAAGAAATGGCACTACTAGATGG 1156  
Db 2463 TGAATTCCTGCTTTTATTTACTGGGCTCGGCTATCAGGGCTCGGCTCCACTCACTGG 2522  
QY 1157 TGTATGATGGGAAGAAACGAGTATCTGAGATGTTATTTATGGGCACTTCGAACCTTAA 1216  
Db 2523 TTTACGATGGGTGGAACAGTTATATTCGCTGTACTTGTCTGTGAAGCCCTCA 2582  
QY 1217 TTACATTTGGTGGCTTCCAGAACCAAACTTTATTTGAAATTTGTTTTTCAACTCTTGA 1276  
Db 2583 TCACCATCGGGGGCTGCTCGACCCCAAGACACTCTTTGAAATTTGTTTCCAGCTGCTGA 2642  
QY 1277 ATTTTCTTGGAGTTTGTGTTCTCCAGTTTAAATTTGGTTCAGATGAGATGTGATG 1336  
Db 2643 ATTTATTTTCCAGGGGCTCTTTCTTCTGTGTGATCGGACAGATGAGATGTGTAG 2702  
QY 1337 GAGCAGCTACAGCCAACTCAGAACTACTTCCGCGCTGATGATGACACCACTTGCCTACA 1396  
Db 2703 GGGCGCCACCGGGACAGACTTACTACCGAGCTGCTGATGGAACGCGTGAAGTACA 2762  
QY 1397 TGAACAAATTAATCTTCAATTTGTCAAAAGCGAGTTTCGGAATTTGGTATGAATATA 1456  
Db 2763 TGAATTTCTACAGATCCCAAGTCCGTCGACACCGCTCAAGACCTGGTACAGTACA 2822  
QY 1457 CATGGACTCTCAAGAATGCTAGATGATGATGCTTGAAGACCTTCAACACTAGCG 1516  
Db 2823 CTTGGCACTCGAAGGCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 2882  
QY 1517 TCCAGTTAGCCTCGCCATTCATGTAATTTGTCAAAAGCGAGTTTCGGAATTTGGTATGA 1576  
Db 2883 TCGGCTGGACTCGCCATCGAGTGAATTTGTCAAAAGCGAGTTTCGGAATTTGGTATGA 1636  
QY 1577 AGGTTGTGATACACAGATGATTTATGACATGTTTGTGTAAGATTTGAAATTCCTCTATT 1636  
Db 2943 AGGCTGTGACCGGCAGATGATTTGACATGCTGAGAGGCTTCGCTCTGTTGCTTACC 3002  
QY 1637 TGCCTGTGATCTTGTCTGCAAAAAGGAGGAAATTTGGCAAGAAATGATATATCATCAAGC 1696  
Db 3003 TGCCCAAGCACTATGTTGCAAGAGGGGGAGATCGGCGGTGAGATGTACATCATCCAGG 3062  
QY 1697 ATGAGAGTCCAAAGTTCTTGGAGCCCTGATGATGATGATGATGATGATGATGATGATG 1756  
Db 3063 CAGGCAAGTGCAGGCTTCTTGGCGGCCCTGATGAGGAAATCTGTGCTGGTACGCTGAAAG 3122  
QY 1757 CTGGGTGGTGTGGGAAATCAGCCTTCTAGCAGCAGGAGGAGGAAACCGTTCGAATCTG 1816  
Db 3123 CTGGATCTGTGTTGGAGAAATAGCTTGTGCTGCTGTTGGGGCGGACCGCGCACGG 3182  
QY 1817 CCAATGTGGTGGCCCAAGGTTTGGCAATCTTTTAACTCTAGACAAAAGACCTTCCAAG 1876  
Db 3183 CCAACGTGGTGGCGCAGGGTTTACCAACCTCTTCACTCTGATGAAGAGGACCTGAATG 3242  
QY 1877 AAATTTCTAGTCATATCCAGATTTCTGAAAGGATCTTCAATGAAGAAAGGAGTGCTTT 1936  
Db 3243 AGATTTTGGTGCATATCTCTAGTCTCAGAGTTTACTCCGGAAGAAAGCCAGCGCATGC 3302

QY 1937 TAAAGCAAGAGGCTAAGACCCGAGAAG 1963  
Db 3303 TGAGAAGCAACAATAAGCCCAAGGAGG 3329  
RESULT 6  
US-10-027-632-204539  
; Sequence 204539, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 204539  
; LENGTH: 680  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(680)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-027-632-204539  
Query Match 12.6%; Score 306; DB 13; Length 680;  
Best Local Similarity 99.7%; Pred. No. 5.9e-56;  
Matches 317; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 2101 CAGAAGAAAGAAATTTCTGAAGGAGGAGAGAGAAAGAAATGAAGATAAACAA 2160  
Db 364 CAGAAGAAAGAAATTTCTGAAGGAGGAGAGAGAAAGAAAGAAATGAAGATAAACAA 423  
QY 2161 AAAGAAATGAAGATAAACAAAGAAATGAAGATAAACAAAGAAATGAAGATAAACAA 2220  
Db 424 AAAGAAATGAAGATAAACAAAGAAATGAAGATAAACAAAGAAATGAAGATAAACAA 483  
QY 2221 GATAAGGAAGAGAGCCAG 2280  
Db 484 GATAAGGAAGAGAGCCAG 543  
QY 2281 ATTCCAGTGGAG 2340  
Db 544 ATTCCAGTGGAG 603  
QY 2341 CGTCAATCACTCATTATCAGCATGGCTCTTCTGCTGAGGCGGAGAGAGAGAGAGAGAG 2400  
Db 604 CGTCAATCACTCATTATCAGCATGGCTCTTCTGCTGAGGCGGAGAGAGAGAGAGAG 663  
QY 2401 ATTGAAGTCAAGAGAAAG 2418  
Db 664 A-TGAAGTCAAGAGAAAG 680  
RESULT 7  
US-10-027-632-204539

	Query Match	7.3%	Score 176.4;	DB 17;	Length 2500;
	Best Local Similarity	49.6%;	Pred. No. 1.1e-27;		
	Matches 617;	Conservative 0;	Mismatches 591;	Indels 36;	Gaps 5;
Qy	740	CAGACAACTACACTACTGTGCTTATTGCGGACATCATATGTGATATCATCTACCTTTATG	799		
Db	605	CTGATTACCTAGAAATTTGGCTCATTTTGGATTACGTTATCAGACATAGTCTATTTAATCG	664		
Qy	800	ATATGCTATTTATCCAGCCOCAGACTCCAGTTTGTAAAGAGGAGGAGACATATATAGTGGATT	859		
Db	665	ATATG---TTTGTACGAACAAGGCACAGTTTACCTAGAAACAAGGACTGCTGTGTAAGGAAG	721		
Qy	860	CAAAATGAGCTAAGGAACAACATACAGGACTTCTACAAAATTTTCAGTTGGATGTGCGCATCAA	919		

	D	722	AACCTTAAATCATTAATAAATAATATCCCAACTTCGCAATTAGACATGGATGTCTGTC	781
QY		920	TAATACCAATTTGAATATTTGCTACCTCTCTTTGGGTTTA--ATCCAATGTTTTAGACAA	976
D				
D		782	TGATACCACCTGATTTGCTGTATTTTAAAGTTAGGGTGGAACTATCCAGAAATTAGATTAA	841
QY		977	ATAGGATGTTAAAGTACACTTCATTTTTCGAAATTTAATCATCACCTTAGAGTCTTATATGG	1036
D		842	ACAGGTGTTTACCGTCTCTCGTATGTTTGAGTCTTCCAGAGAACAGAACAAGGCACAA	901
QY		1037	ACAAAGCATAATCTACAGAGTTTATTCGAACAACACTGGATCTTGCTGTTTATTTCTGCACA	1096
D		902	ACTATCCAAACATCTTCAGGATTTCCAAACCTTGTTATGATATCGTCATCATTTCCACT	961
QY		1097	TTAATGCCGTGTTTATTTACTTGGCGTTCAAACCTATGAGAGAAATTTGGCACTACTAGATGG	1156
D				
D		962	GGAATGCATGTGTGTTCTACTCTATTTCTAAAGCTATTTGGATTTGGAAATGATACATGGG	1021
QY		1157	TGTA-----TGATGGGAAGGAAACGAGTACTCGAGATGTT	1192
D		1022	TCTACCTGATATTAATGATCCTGAATTTGGCGTTGGCTAGAAAATACGTATACAGCC	1081
QY		1193	ATTATTTGGGCAGTTCCGAACCTTTAATTAACCATTTGGTGGCCTCCAGAACCAACAACCTTTAT	1252
D		1082	TTTACTGGTCTACACTGACTTTGACTACCATTTGGTGAACAACCCCTCCCGTGAGGGATT	1141
QY		1253	TTGAAATGTTTTTCAACTCTTGAATTTTTTTCTCGAGTTTTTTGTTCTCCAGTTTAA	1312
D		1142	CTGAGTATGCTTTGTGGTGTTGATTTCCCTAATTTGGAGTGTTAATTTTTTGTCTACCATCG	1201
QY		1313	TTGGTCAGATGAGAGATGTAITGGAGCAGCTACAGCCAATCAGAACTACTTCCGGCGCT	1372
D		1202	TTGGTAACTAGGTTCTATGATTTCCAAACATGAATGCAGCCAGCAGAGAATTTCAAGCAA	1261
QY		1373	GCATGATGACACCATTTGCCCTACATGAACAAATTTACTCCATTTCTCTAAACTTTGTGCAAAAGC	1432
D		1262	GAAATTGATGCTATCAAGCAATATATGCATTTTCGAAATGTAAAGCAAGAATATCGAAAAGA	1321
QY		1433	GAGTTCGGACTTGGTATGAATATACATGGCACTCTCAAAGAATTCGTAGATGAGTCTGATT	1492

Qy	1313	TTGGTCAGATGAGAGATGATTTGGAGCAGCTACAGCCAACTCAGAACTACTTCCGGCGCT	1372
Db	1202	TTTGGTAACATAGGTTCTATGATTTCCAACTAGTATGCGCAGCAGCAAAATTTCAAGCAA	1261
Qy	1373	GCATGGATGACACCAATTGGCTACATGAACAAATTAATCCATTCCTAAACTTGTGCAAAAGC	1432
Db	1262	GAATTCATGCTATCAAGCAATATATGCAATTTTCGAAATGTAAACCAAGATATATGAAAAGA	1321
Qy	1433	GAGTTCGGAGCTTGGTATGAATATACATGCGACTCTCAAAGAAATGCTAGATGAGTCTGATT	1492

Db 1322 GGGTTATTAAATGGTTGACTACCTGGACCAACAAAAACAGTTGATGAGAAG 1381  
 Qy 1493 TGCTTAAGACCCCTACCAACTACGGTCCAGTTAGCCCTGCCATTGATGTGAATTCAGCA 1552  
 Db 1382 TCTTAAAGTATCTACTGATTAACAAAGGAGCAAAATGGCCATCAAGCTTCACTTAGACA 1441  
 Qy 1553 TCATCAGCAAGTCGACTGTGTTCAAGGGTGTGATACACAGATGATTTATGACATGTTGC 1612  
 Db 1442 CATTAAAAAGGTACGCATTTTGTGATTTGTGAAGCTGGTCTGTGGTGGAGTTGGTCT 1501  
 Qy 1613 TAAGATTGAATCCGTTCTCTATTGTCCTGGTGACTTTGTCTGCAAAAGGGAGAAATG 1672  
 Db 1502 TGAATTTGAACCCCAAGCTCTACAGTCTGGAGATTTATTTGCAAGAAAGGGGATNCG 1561  
 Qy 1673 GCAAGGAATGTATATCAAGCATGGAGAGTCCAAGTTCTTGGAGCCCTGATGGTA 1732  
 Db 1562 GACGAGAGATGATACATTCAAGGAGCAAACTCGTGTGGCGCATGATGGAGTCA 1621  
 Qy 1733 CTAAAGTTCTGGT-----TACTCTGAAGCTGGGTGGTGGTGGAGAAATC--AGCCTTC 1786  
 Db 1622 CTCAGTTTGTGATTTAGCGATGGCAGCACCTTCGGTGAGATCAGCATTTCTTAACATTA 1681  
 Qy 1787 TAGCAGCAGGAGGAGAAACCTGCAACTGCCAATGTGGTGGCCACCGGTTTGCCAATC 1846  
 Db 1682 AAGGAGCAAGCTGGCAATCGAAGACGGCCCAATTTAAAGTATTTGGCTACTCAGACC 1741  
 Qy 1847 TTTTAACTCTAGACAAAAAGCCCTCCAAAGAAATCTAGTGCAATTCAGATTCAGAA 1906  
 Db 1742 TGTCTGTCTCTCAAGATGACCTCAGGAGCTCTAAGTGTACCAAGTACCAAGTCCAAA 1801  
 Qy 1907 GGATCCTCATGAAGAAAGCCAGAGTGTCTTTTAAAGCAGAAGCT 1950  
 Db 1802 CTATGCTAGAAGAAAAAGGGAAGCAAAATTTTAAATGAAAGATGGT 1845

RESULT 9

US-10-342-887-427  
 ; Sequence 427, Application US/10342887  
 ; Publication No. US20040058340A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dai, Hongyue  
 ; APPLICANT: He, Yudong  
 ; APPLICANT: Linsley, Peter S.  
 ; APPLICANT: Mao, Mao  
 ; APPLICANT: Roberts, Christopher J.  
 ; APPLICANT: Van 't Veer, Laura Johanna  
 ; APPLICANT: Van de Vijver, Marc J.  
 ; APPLICANT: Bernards, Rene  
 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
 ; FILE REFERENCE: 9301-188-999  
 ; CURRENT APPLICATION NUMBER: US/10/342,887  
 ; PRIORITY FILING DATE: 2003-01-15  
 ; PRIOR APPLICATION NUMBER: 60/298,918  
 ; PRIOR FILING DATE: 2001-06-18  
 ; PRIOR APPLICATION NUMBER: 60/380,710  
 ; PRIOR FILING DATE: 2002-05-14  
 ; PRIOR APPLICATION NUMBER: 10/172,118  
 ; PRIOR FILING DATE: 2002-06-14  
 ; NUMBER OF SEQ ID NOS: 2699  
 ; SEQ ID NO 427  
 ; LENGTH: 2500  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-342-887-427

Query Match 7.3%; Score 176.4; DB 17; Length 2500;  
 Best Local Similarity 49.6%; Pred. No. 1.1e-27;  
 Matches 617; Conservative 0; Mismatches 591; Indels 36; Gaps 5;  
 Qy 740 CAGACACATACACTACTGGCTTATTTGGGAGCATCATGTGATCATCTACCTTTATG 799  
 Db 605 CTGATTACCTAGAATATTGGTCTATTTGGATTTAGCTATCAGACATAGTCTATTAAATCG 664

Qy 800 ATATGCTATTATCCAGCCAGACTCCAGTTTGTGAAGAGGAGACATAATAGTGGATT 859  
 Db 665 ATATG---TTTGTAGCAACAAGGACAGGTTACCTAGAACAAAGGACTGCTGGTAAAGGAAG 721  
 Qy 860 CAAATGAGCTAAGGAAACACATACAGGACTTCTACAAAATTTTCAGTTGATGTCGATCAA 919  
 Db 722 AACTTAAACTCATAAATAAATAAATCCAACTTTGCAATTTTAAACTTGTATGTTCTGTGAC 781  
 Qy 920 TAATACCATTTGATATTTGCTACCTCTCTTTTGGGTTTA---ATCCAATTTTGTAGAGAA 976  
 Db 782 TGATACCAACTGATTTGCTGTATTTAAAGTTAGGGTGGAACTATCCAGAAATTTAGATTAA 841  
 Qy 977 ATAGAGTGTAAAGTACACTTTCATTTTGTGAATTTAATCATCACCTAGAGTCTATAATGG 1036  
 Db 842 ACAGTTTGTACGGTCTCTCGTATGTTGAGTTCTTCCAGAGAACAAGGACAA 901  
 Qy 1037 ACAAGCATATATCTACAGAGTTATTCGAACAACCTGGTACTTGTGTTTATTTCTGACACA 1096  
 Db 902 ACTATCCAAACATCTCTCAGGATTTTCCAACTTTGTTATGTATATCGTCACTATTCCTACT 961  
 Qy 1097 TTAATGCTGTGTTTATTTACTGGGCTTCAAACTATGAAGAAATTTGGCACTACTAGATGG 1156  
 Db 962 GGAATGCATGTGTGTTCTACTCTATTTCTAAAGCTATTTGGAAATGATACATGCG 1021  
 Qy 1157 TGTA-----TGATGGGAGGAAACGAGTATCTGAGATGTT 1192  
 Db 1022 TCTACCTCGATATTAATGATCCTGAAATTTGGCCGTTTGGCTAGAAAAATACGTATACAGCC 1081  
 Qy 1193 ATTAATGGGAGTTCGAACTTTAATTAATTTGTTGGCTTCCAGAACCAAACTTTAT 1252  
 Db 1082 TTTACTGCTCTACACTGACTTTTGTACCAATTTGGTGAACACCCCTCCCGTAGGGATT 1141  
 Qy 1253 TTGAAATTTGTTTCAACTCTTGAATTTTCTGGAGTTTGTGTTCTCCAGTTTAA 1312  
 Db 1142 CTGATGATGTTTGTGGTGGTGTGATTTCTTAATTTGGAGTGTAAATTTTGTCTACATCG 1201  
 Qy 1313 TTGCTCAGATGAGAGATGTGATTTGGAGCAGCTACAGCCAAATCAGAACTACTTCCCGGCT 1372  
 Db 1202 TTGGTAAACATAGTTCTATGATTTTCCAACATGAATGCAGCCAGAGCAGAAATTTCAAGCA 1261  
 Qy 1373 GCATGGATGACACCATTTGCCCTACATGAACAATTTACTCCATTTCTTAACTTTGTGCAAAAGC 1432  
 Db 1262 GAATTTGATGCTATCAAGCAATATATGCAATTTTCAAAATGTAAAGCAAGATATGAAAAAGA 1321  
 Qy 1433 GAGTTTCGACTTGTGATGAATATACATGGGACTCTCAAAGAAATGCTAGATGATCTGAT 1492  
 Db 1322 GGGTTATTAAATGGTTTGTACTCTGTGGACCAACAAAAAACAGTTGATGAGAAAGAG 1381  
 Qy 1493 TGCTTAAAGACCTTACCAACTACGGTCCAGTTTAGCCCTCGCCATTTGATGTGAATTCAGCA 1552  
 Db 1382 TCTTAAAGTATCTACTGATTAACACTAAGAGCAGAAATTTGCCATCAACGTTCTACTTAGACA 1441  
 Qy 1553 TCATCAGCAAGTGCAGCTTTGTTCAAGGGTGTGATACACAGATGATTTATGACATGTTGC 1612  
 Db 1442 CATTAAAAAGGTACGCATTTTCTGCTGATGTGAAGCTGGTCTGTGGTGGAGTTGGTCT 1501  
 Qy 1613 TAAGATTGAATCCGTTCTCTATTGCTGTGAGTCTTGTCTGCAAAAGGGAGAAATG 1672  
 Db 1502 TGAATTTGCAACCCCAAGCTCTACAGTCTTGAGATTTATTTTGAAGAAAGGGGATATCG 1561  
 Qy 1673 GCAAGGAATGTATATCATCAAGCATGGAGAAATTCAGATTTCTTGGAGCCCTGATGGTA 1732  
 Db 1562 GACGAGAGATGATCATTTATCAAGGAAGCAAACTCGCTGTGGTGGCAGATGATGGAGTCA 1621  
 Qy 1733 CTAAAGTTCTGGT-----TACTCTGAAGCTGGGTGGTGGTGGAGAAATC--AGCCTTC 1786  
 Db 1622 CTCAGTTTGTGATTTAGCGATGGCAGCACCTTCGGTGAGATCAGCATTTCTTAACATTA 1681  
 Qy 1787 TAGCAGCAGGAGGAGAAACGTCGAACTGCCAATGTGGTGGCCACCGGTTTGCCAATC 1846  
 Db 1682 AAGGAGCAAGCTGGCAATCGAAGACGGCCCAATTTTAAAGTATTTGGCTACTCAGACC 1741











?	OTHER INFORMATION:				
US-10-087-217-5	Query Match	5.4%;	Score 131.6;	DB 15;	Length 1995;
	Best Local Similarity	46.7%;	Prod.No. 5e-18;		
	Matches 622;	Conservative 0;	Mismatches 674;	Indels 36;	Gaps 5;
Qy	652	TATCTCTGTGGCTCTTGCTGTGTCACCTCTTGGCCTATAACTGAACCTGCTGTTTATACCA	711		
Db	424	TATTACGGTTGGTTGTTGTGTCATTGGCATGCCCTGTTCTTTACAACGGTGCCTGTTGGTG	483		
Qy	712	CTGGGCGCTGCTTCCCATATCAAAACGGCAGACAACATACACTACTGCTGGCTTATTGCGGAC	771		
Db	484	GCCAGAGCCCTGCTTCAGTGTGATCTACAGAGAAAATATTTTGTGGTATGGCTGGTCTGGAC	543		
Qy	772	ATCATATGTGATATCATCTACCTTTTATGATATGCTATTTATTCAGCCACGACTCCAGTTT	831		
Db	544	TACTTCTCAGACACTGTCTATATCGCAGACCTCATCATTCGGCTGGCAGAGG---TTC	600		
Qy	832	GTAAAGGAGGAGACATAATAGTGGATTCAAAATGAGCTAAGGAACACTACAGGACTTCT	891		
Db	601	CTAGAACAGGGCTCTTGGTCAAAGATCCCAAGAAATTCGAGACAACATATATTCACACT	660		
Qy	892	ACAAAATTTTCAGTTGGATGTCGATCAATAATACCAATTTGATATTTGCTACTCTCTTTT	951		
Db	661	TTGCAGTTCAAAATTTGGATGTTGGCTTCTATCATTTCCCACTGACCTATCTATTTTGTGTG	720		
Qy	952	GGGTT---TAATCCAATGTTTAGAGCAATAGGATGTTAAAGTACACTTCATTTTGTGAA	1008		
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Qy	1009	TTTAAATCATCACCTAGAGTCTATAATTTGGACAAAGCATATATCTACAGAGTTATTCGAACA	1068		
Db	781	TTCTTTTGACCGCACTGAGACACGCAACGACTACCCCAACATCTTCCGAATCAGCAATCTG	840		
Qy	1069	ACTGGAATACTTGCTGTTTATTTGCAATTAATAGCTGTGTTTATTTACTGGGCTTCAAAC	1128		
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Qy	1129	TATGAAGGAATTGG-----CACTACTAGATGGGTGATGAT	1164		
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Qy	1165	GGGGAAGGAAACAGATATCTGAGATGTTATTTATGGGCAGTTTCCAACTTTAAATACCATT	1224		
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Db	1381	GAAGCTGGCCTA	CTAGTGGTGGAACTCGGTACTGAAAGCTTCGTCTCGTCTAGGTCCTTTAGTCTCTGGA	1444
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; Sequence 2, Application US/10295573				
; Publication No. US2003015751A1				
; GENERAL INFORMATION:				
; APPLICANT: Karpen, Jeffrey W.				
; APPLICANT: Rich, Thomas C.				
; APPLICANT: Cooper, Dermot M.F.				
; APPLICANT: Schaaack, Jerome				
; TITLE OF INVENTION: MODIFIED CYCLIC NUCLEOTIDE GATED ION CHANNELS				
; FILE REFERENCE: UTC-07536				
; CURRENT APPLICATION NUMBER: US/10/295,573				
; CURRENT FILING DATE: 2002-11-15				
; PRIOR APPLICATION NUMBER: 60/332,494				
; PRIOR FILING DATE: 2001-11-16				
; NUMBER OF SEQ ID NOS: 8				
; SOFTWARE: PatentIn version 3.1				
; SEQ ID NO 2				
; LENGTH: 3027				
; TYPE: DNA				
; ORGANISM: Rattus norvegicus				
US-10-295-573-2				
Query Match 5.4%; Score 131.6; DB 16; Length 3027;				
Best Local Similarity 46.7%; Pred. No. 6.1e-18;				
Matches 622; Conservative 0; Mismatches 674; Indels 36; Gaps 5;				
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Qy	712	CTGCGCCTCGTCTTCCCATATCAAAACCGCAGACAACA	TACACTCTGGCTTTATGCGGAC	771
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Qy	772	ATCATATGTGATATCATCTACCTTTATGATATGCTATT	TATCCAGCCCACTCCAGTTT	831
Db	883	TACTTCTCAGACACTGTCTTATATCGCAGACCTCAT	CTATCGGCTGGCGCAGGC---	939
Qy	832	GTAAGAGGAGGAGACATAAATAGTGGATTTCAAT	TGAGCTTAAGGAAACACTACAGGACTTCT	891
Db	940	CTAGACAGGGGCTTCTTGGTCAAGATCCCAAGAAAT	TGGAGACAACATATATTCACACT	999
Qy	892	ACAAATTTTCAGTTGGATGTGCGCATCAATAATACCA	TTTGATATTTGCTACCTCTCTTT	951
Db	1000	TTGCAGTTTCAAAATTTGGATGTGGCTTCTATCATTT	CCCACTGACCTTATCTATTTTGGTGTG	1059

Qy	952	GGGTT---TAA	TC	CAATGTTT	AG	CAAAAT	AG	ATGTTT	AAAGT	TAC	ATCTT	CA	TTTTTT	GTAA	1008
Db	1060	GGTATCC	ACAGCCCT	CAGGT	TACGCTT	CAAC	CGGCT	TATTA	TACATCTT	CCGCCG	TATGTT	TGAG	1119		
Qy	1009	TTTAAAT	CATCACCT	TAGAGT	CTATAA	TGGCAAA	AGCATATATCT	TACAGAGT	TATATTC	GAAACA	1068				
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Db	1180	GTCCTT	TACATCTT	GGTTCAT	CTCCTG	ATCATCC	ACTGGAATGCTT	GTTATTTAT	TATGTT	ATTTCTT	CTAAG	1239			
Qy	1129	TATGA	AGGAATGG	-----	-----	-----	-----	CACTACT	AGATGGG	TGTATGAT	1164				
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Qy	1165	GGGAA	AGGAAAC	GAGTATCT	GAGATG	TATTAATT	TGGGCAGTTC	CGAACTTT	TAATTA	TACCATT	1224				
Db	1300	TACCT	GGCTAG	AGGTACATTT	TACTGTC	TACTGGT	CCACACT	TGACCCCT	CACCA	CAAT	1359				
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Qy	1285	TC	TGGAGTTT	TCTGTTT	CTCCAGT	TTTAAT	TGGTCAGAT	TGAGAGAT	GTGAT	TGGAGCAGCT	1344				
Db	1420	ATTGG	TGCTCATCTT	TGCCAT	TATTTG	TGGGAAATG	TGGGCTC	CAATGATCT	CCACATG	1479					
Qy	1345	ACAGC	CAATCAG	AACTACTT	CCGCGCT	GCATGG	ATGACACCA	ATGCTT	GCCTAC	TGAAACAAT	1404				
Db	1480	AATGCC	ACACGAG	CAGATTCC	AGGCCAA	AGATTGAT	GCTGTCAA	ACACTAC	ATCATG	CACTG	1539				
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Qy	1525	GC	CTTCC	CAATGAT	GTGAACTT	CAGCAT	CATCAG	CAAAAGT	TGCACTTGT	TCAAGG	TTGT	1584			
Db	1660	GAG	ATAG	CCATTAAT	GTTTCA	CTTGT	CCACTCTG	AAAGAAATG	CGCATAT	TCCAG	GAATGG	1719			
Qy	1585	GAT	ACACAG	ATGATTTAT	GACATG	TGTTGCTT	TAAGAT	TGAAATCC	GTCTCTAT	TGTCCTGGT	1644				
Db	1720	GA	AGCTGG	CCCTACT	GGTGG	AACTGGT	TACTG	AGCTTC	GTCTCCTC	AGGCTTT	TAGTCT	1779			
Qy	1645	GAC	TTTTGT	CTGCAAA	AGGGAG	AAATTTG	GC	AAAGAAAT	GTATAT	ATATCA	AGCAT	1704			
Db	1780	GAT	TATATT	TG	CCGTAA	GGGGACA	TTGGCA	AGAAATGT	ATCATAT	CAAGG	AGGCAAG	1839			
Qy	1705	GT	CCAAGTCTT	GGAGCCCT	GTATG	TACT	ATAAGT	TTCTGGT	----	TACTCT	GAAAGCTG	1760			
Db	1840	TT	GGAGTGGT	AGCTCAT	ATGATGG	CGTACT	AGTATG	CCCTTG	CTCTC	TAGCTGG	AGGAGCTG	1899			
Qy	1761	GT	CGGTTTTT	GGAGAAAT	CAGCCCTT	CAGCAG	CAGGAGGA	--	GGAAAC	CGT	CGAACTGCC	1818			
Db	1900	TT	TGGTGAG	ATTAGTAT	CCCTTA	CAATTAAG	GGGTAG	CAAAAT	TGGCAAT	CGAGT	ACTGCT	1959			
Qy	1819	AAT	TGGTGG	CCCA	CGGTTT	TGGCAATCT	TTTTAACT	CTAG	ACHAAA	AGACCC	TCCAGAA	1878			
Db	1960	AAT	ATCCGT	AGCCTGG	GGCTACT	CAGATCTCT	CTCTG	CTTGT	TCC	AAAGCAG	ATCTTAT	2019			
Qy	1879	ATT	CTAGT	GCATTTAT	CCAGAT	TTCTG	AAAGG								

Search completed: March 27, 2005, 20:53:32  
Job time : 1286 secs

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GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: March 27, 2005, 10:55:09 ; Search time 7048 Seconds  
(without alignments)  
13123.748 Million cell updates/sec

Title: US-09-855-828-3

Perfect score: 2430

Sequence: 1 atgtttaatcgtgacaaa.....aagaagaaggtaagaataa 2430

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gsa1:\*

9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	815.8	33.6	2056	3 AK040140	AK040140 Mus muscu
2	553	22.8	553	2 BF725470	BF725470 bx16c03.y
3	478	19.7	527	1 AL713036	AL713036 DKEP686A
4	477.4	19.6	1947	3 CR626336	CR626336 full1-len
5	470	19.3	655	2 BB635459	BB635459 full1-len
6	430.2	17.7	437	2 BF725469	BF725469 bx16c03.x
7	402.4	16.6	881	2 BE287002	BE287002 601097229
8	363.8	15.0	1054	5 BX401127	BX401127 BX401127
9	320.8	13.2	468	1 AA069559	AA069559 zf75a04.r
10	320.8	13.2	656	5 BP224184	BP224184 BP224184
11	308.4	12.7	978	5 BQ068992	BQ068992 AGENCOURT
12	304	12.5	633	7 CK619966	CK619966 mk30e03.y
13	301.4	12.4	694	1 AU137778	AU137778 AU137778
14	286.8	11.8	741	5 BX104558	BX104558 BX104558
15	280.8	11.6	738	4 BI736222	BI736222 603359912
16	280	11.5	423	5 BM938767	BM938767 UI-N-CGOp
17	279	11.5	445	7 H53423	H53423 YF86a09.r1
18	277.6	11.4	747	7 CR376265	CR376265 CR376265
19	271.2	11.2	545	2 AW465556	AW465556 BP230019A
20	262.2	10.8	563	4 BG304577	BG304577 f188b05.y
21	261.6	10.8	503	1 AI150392	AI150392 qf40g11.x
22	234	9.6	247	1 AA317961	AA317961 EST20020
23	232.4	9.6	270	1 AA012972	AA012972 ze35b03.r
24	224	9.2	325	2 BE982488	BE982488 UI-N-CGOp

25 219.6 9.0 823 7 CO814239 AGENCOURT  
26 219 9.0 696 5 BW269181 BW269181  
c 27 216.2 8.9 518 1 AV605886 AV605886  
28 216.2 8.9 747 4 BI733974 BI733974 603355503  
29 212.4 8.7 215 1 AA069498 AA069498 zf74e07.r  
30 211 8.7 869 6 CD327412 AGENCOURT  
31 201.6 8.3 979 5 BX370500 BX370500  
32 197.2 8.1 581 1 AV605887 AV605887  
33 165.6 6.8 353 1 AL120448 AL120448 DKEP27611  
34 164 6.7 376 1 AL120239 AL120239 DKEP2761H  
35 163.4 6.7 725 7 CR371016 CR371016  
c 36 162.2 6.7 674 9 CC498739 CH240 335  
37 137 5.6 832 4 BI827605 BI827605  
c 38 131.2 5.4 591 9 CC571022 CH240 446  
39 129.8 5.3 573 4 BM354832 BM354832 rr17e02.y  
c 40 120.6 5.0 535 1 AL928461 AL928461  
41 111 4.6 920 5 BU139545 BU139545 603133625  
42 110.6 4.6 490 5 BQ633921 BQ633921 he21h09.y  
c 43 109.2 4.5 584 5 BM882371 BM882371 ra99h10.y  
44 108.8 4.5 777 7 CK477930 AGENCOURT  
45 106.8 4.4 819 5 BU287884 BU287884 603603670

## ALIGNMENTS

RESULT 1  
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LOCUS AK040140 2056 bp mRNA linear HTC 03-APR-2004  
DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430069G05 product:cyclic nucleotide gated channel beta 3, full insert sequence.  
ACCESSION AK040140.1 GI:26087649  
VERSION AK040140.1  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1  
AUTHORS Carninci,P. and Hayashizaki,Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
REFERENCE 2  
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 11042159  
PUBMED 1042159  
REFERENCE 3  
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kaehiwaiki,K., Fujiwaka,S., Inoue,K., Togawa,I., Izawa,M., Ohara,E., Wachiaki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillar sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861  
REFERENCE 4  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
PUBMED 11076861  
REFERENCE 5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research



RESULT 2  
BF725470  
LOCUS  
DEFINITION  
bxi16c03.y1 Human Iris cDNA (Un-normalized, unamplified): BX Homo sapiens cDNA clone bxi16c03 5', mRNA sequence.  
ACCESSION  
BF725470  
VERSION  
BF725470.1 GI:12041381  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1. (bases 1 to 553)  
Wistow, G.J., Bernstein, S., Behal, A. and Smith, D.  
NEIBANK: EST analysis and bioinformatics for ocular genomics Invest. Ophthalmol. Vis. Sci. 41 (2000) In press  
JOURNAL  
COMMENT  
Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov  
Plate: 16 row: c column: 03  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
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## FEATURES

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DEFINITION  
AL713036 527 bp mRNA linear EST 04-SEP-2003  
DKFP8686A1695\_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone  
ACCESSION  
AL713036  
VERSION  
AL713036.1 GI:19696392  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1. (bases 1 to 527)  
AUTHORS  
Bloeker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and Wiemann, S.  
TITLE  
EST (Bloeker, H., Boecker, M., Brandt, P., Mewes, H.W., Weil, B. and Wiemann, S.)  
JOURNAL  
Unpublished (1999)  
COMMENT  
Contact: MIPS  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.  
No 5' sequence available.  
This clone (DKFP8686A1695) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## FEATURES

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/lab\_host="DH10B"  
/clone\_lib="686 (synonym: hlcc3)"  
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cDNA-collection"

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## ORIGIN

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Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 GTTTATTCTGCACATTAAATGCTGTTTATTACTGGCTTCAAACTATGAAGNAATGG 60  
Qy 1143 CACTACTAGATGGGTGATATGCGGAAGGAAACGAGTATCTGAGATCTTATTATTGGGC 1202  
Db 61 CACTACTAGATGGGTGATATGCGGAAGGAAACGAGTATCTGAGATCTTATTATTGGGC 120  
Qy 1203 AGTTTCAACTTTAATACCATTTGGTGGCTTCCAGAACCAAACTTTATTGAAATGT 1262  
Db 121 AGTTTCAACTTTAATACCATTTGGTGGCTTCCAGAACCAAACTTTATTGAAATGT 180  
Qy 1263 TTTTCAACTCTGAATTTTTTTCTGGAGTTTTTGTGTCTCCAGTTAAATGGTCAGAT 1322  
Db 181 TTTTCAACTCTGAATTTTTTTCTGGAGTTTTTGTGTCTCCAGTTAAATGGTCAGAT 240





QY 1881 TCTAGTCATTATCCAGATTCTGAAGGATCTCATGAAGAGCCAGAGTCCTTTTAAA 1940  
 Db |||||  
 1024 TTGTGTCATTATCTGTAGTCTCAAGATTACTCCGGAAGAACCCAGCGCATCTGAG 1083  
 QY 1941 CGAAGAGCTTAAGACCGCAGAG 1963  
 Db |||||  
 1084 AAGCACATAAGCCCAAGGAGG 1106

RESULT 5  
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 LOCUS BB635459 RIKEN full-length enriched, 0 day neonate thymus Mus  
 DEFINITION musculus cDNA clone A430069G05 5', mRNA sequence.

ACCESSION BB635459  
 VERSION BB635459.1 GI:16471509  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 655)

AUTHORS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,  
 Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,  
 Konno, H., Kouda, N., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,  
 Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,  
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,  
 Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

TITLE Unpublished (2001)  
 JOURNAL Contact: Yoshihide Hayashizaki  
 COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222

Fax: 81-45-503-9216  
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
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 prepare full-length cDNA libraries for rapid discovery of new  
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 and Hayashizaki, Y.

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 Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and  
 Hayashizaki, Y.  
 Computational Analysis of Full-length Mouse cDNAs Compared with  
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)  
 Please visit our web site (http://genome.gsc.riken.go.jp) for  
 further details.

e mouse tissues.

FEATURES Location/Qualifiers

1..655  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
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 /clone="A430069G05"  
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/clone\_lib="RIKEN full-length enriched, 0 day neonate  
 thymus"  
 /note="Site 1: Sali; Site 2: BamHI; cDNA library was  
 prepared and sequenced in Mouse Genome Encyclopedia  
 Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in  
 RIKEN. Division of Experimental Animal Research in Riken  
 contributed to prepare mouse tissues. 1st strand cDNA was  
 primed with a primer [5'  
 GAGAGAGAGAGATCCAAAGAGCTCTTTTCTTTTNN 3'], cDNA was  
 prepared by using trehalose thermo-activated reverse  
 transcriptase and subsequently enriched for full-length by  
 cap-trapper. cDNA went through one round of normalization  
 to Rot = 10.0 and subtraction to Rot = 459.0. Second  
 strand cDNA was prepared with the primer adapter of  
 sequence [5' GAGAGAGATTCGAGTAAATTAATATCCCTCCCCCCCC  
 3']. cDNA was cleaved with XhoI and BamHI. Vector: a  
 modified pBluescript KS(+) after bulk excision from Lambda  
 FLX I."

# ORIGIN

	Query Match	Score	DB 2;	Length
	Best Local Similarity	84.2%	Pred. No. 2e-98;	
	Matches	553;	Mismatches	0;
	Conservative	101;	Indels	3;
	Gaps	2;		
QY	1078	TTGCTGTTTATTCGCACATTAAATGCGCTGCTTTTATTACTGGGCTTCAAACTATGAAGGA	1137	
Db	1	TTGCTGTTTCTCTCGCACATTAAACGCTGCTTTATTACTGGGCTTCAAGACTATGAAGGA	60	
QY	1138	ATTGGCCTACTAGATGGTGTATGATGGGAAGAAAGAGATCTCAGATGTTATTAT	1197	
Db	61	ATTGGCTCAACTAAATGGGCTCTATAATGGTGAAGGCAACAAGTATCTCGATGCTTTTAT	120	
QY	1198	TGGCAGTTCCAACTTTAATTAATACCATTTGCTGGCTTCCAGAACCAACAATTTTATTCGA	1257	
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QY	1258	ATTGTTTTTCAACTCTTGAATTTTTTTTCTGGAGTTTTTGTGTTCTCCAGTTTAAATGGT	1317	
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QY	1318	CAGATGAGATGATGATGAGAGAGCTACAGCCAAATCAGAACTACTTCCGGCGCTGATG	1377	
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QY	1378	GATCACACCTTGGCTTACATGAAACAATTAATTAATTAATTAATTAATTAATTAATTAAT	1437	
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Db	361	CGGACTTGGTGGAAATATACATGGAACTCAAAAGAAATGCTAGATGCTTGTATGCTT	420	
QY	1498	AAGACCTTACCAACTAGCGTCCAGTACCCCTCCGCAATGATGTAACCTCAGCATCATC	1557	
Db	421	GAGAACCTTCCGACAGCAATGACGTGTCTATTGCCCTTGACATAAACTTCAGTATCATC	480	
QY	1558	AGCAAGTCGACTTTTCAGAGGTTGTGATACAGATGATTATGATCATGCTCTGATAGA	1617	
Db	481	GACAAGTGGAGTTATTCAAGGGCTGTGACACACAGATGATTATGATCATGCTCTGATAGA	540	
QY	1618	TTGAAATCCGTTCTCTATTGTCCTGGTGGTCTTGTCTGCAAAAGGAGAAATTTGGCAAG	1677	
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QY	1678	GAAATGATATATCAAGCATGGAGAGTCAAGTCTTTGGAGGCCCTTGATGGTACT	1734	
Db	601	--AATGTACATCATCAA--CACGGAGAGTCCAAGTCTCTTGGAGGCCCTTGATGGTACT	654	

RESULT 6  
 BF725469/c  
 LOCUS BF725469 437 bp mRNA linear EST 05-JAN-2001

DEFINITION bx16c03.x1 Human Iris cdna (Un-normalized, unamplified): BX Homo sapiens cdna clone bx16c03 3', mRNA sequence.

ACCESSION BF725469

VERSION BF725469.1 GI:12041380

KEYWORDS EST.

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 437)

AUTHORS Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.

TITLE NEIBANK: EST analysis and bioinformatics for ocular genomics

JOURNAL Invest. Ophthalmol. Vis. Sci. 41 (2000) In press

COMMENT Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov  
Plate: 16 row: c column: 03  
Seq primer: -21M13 forward primer (ABI).  
Location/Qualifiers  
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/tissue\_type="iris"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/clone\_lib="Human Iris cdna (Un-normalized, unamplified): BX"  
/note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris tissue was pooled from 10 individuals ranging in age from 4-80 years and RNA was extracted. From this pooled sample an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A directionally cloned cdna library in the pCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (<http://www.lifetech.com/>). First strand synthesis was carried out using a Not I primer-adaptor  
[5'-pGACTAGTCTTAGATCGGCGCGGCC(7)15-3']. Not I/blunt end inserts were cloned into the Not I/EcoR V sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 17.7%; Score 430.2; DB 2; Length 437;  
Best Local Similarity 99.3%; Pred. No. 3.5e-89;  
Matches 432; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1759 GGCTCGGTGTTTGAGAAATCAGCCCTTCTAGCAGCAGGAGGAGAAACCGTCGAATGCC 1818

DB 437 GGCTCGGTGTTTGAGAAATCAGCCCTTCTAGCAGCAGGAGGAGAAACCGTCGAATGCC 378

QY 1819 AATGTGTGCCCCACGGTTGGCAATCTTTAACTCTAGCAAAAAGACCCCTCAAGAA 1878

DB 377 AATGTGTGCCCCACGGTTGGCAATCTTTAACTCTAGCAAAAAGACCCCTCAAGAA 318

QY 1879 ATTCTAGTCATTATCCAGATCTGAAAGGATCCTCATGAAGAAAGCAGAGTGCCTTTTA 1938

DB 317 ATTCTAGTCATTATCCAGATCTGAAAGGATCCTCATGAAGAAAGCAGAGTGCCTTTTA 258

QY 1939 AAGCAGAAGGCTAAGACCGCAGAAAGCAACCCCTCCAAGAAAGATCTTGCCTCTCTTC 1998

DB 257 AAGCAGAAGGCTAAGACCGCAGAAAGCAACCCCTCCAAGAAAGATCTTGCCTCTCTTC 198

QY 1999 CCACCGAAGAAGAGACACCCAACTGTTTAAACTCTCTAGAGGCACAGGAAAGCA 2058

DB 197 CCACCGAAGAAGAGACACCCAACTGTTTAAACTCTCTAGAGGCACAGGAAAGCA 138

QY 2059 AGTCTTGCAGACTACTCAAATTTGAAGCGAGAGCAGCTCAGAGAAAGAAAATTTCT 2118

DB 137 AGTCTTGCAGACTACTCAAATTTGAAGCGAGAGCAGCTCAGAGAAAGAAAATTTCT 78

QY 2119 GAAGGAGGAG 2178

DB 77 GAAGGAGGAG 18

QY 2179 CAAAAGAGAAATGAA 2193

DB 17 CAAAAGAGAAATGAA 3

RESULT 7

LOCUS BE287002

DEFINITION 601097229F1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:3496015 5', mRNA sequence.

ACCESSION BE287002

VERSION BE287002.1 GI:9165707

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 881)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
DNA distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM8547 row: i column: 08  
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Location/Qualifiers  
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/clone\_lib="NCI CGAP Mam5"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Salt; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

FEATURES

source

Query Match 16.6%; Score 402.4; DB 2; Length 881;  
Best Local Similarity 73.9%; Pred. No. 1.2e-82;  
Matches 548; Conservative 0; Mismatches 171; Indels 23; Gaps 2;

QY 1459 TGGGACTCTCAAGAATGCTAGATGATCTGATTTGCTTAAAGACCCCTACCACTACGGTC 1518

DB 1 TGGAACTCAAGAATGCTAGATGATGATCTGATTTGCTTAAAGACCCCTCCGACGAGATG 60

QY 1519 CAGTTAGCCCTCGCCATTTGATGTGAACCTTCAAGATCATCAGCAAGTCGATTTTCAAG 1578

DB 61 CAGTTGTCTATTGCCCCCTTGACATAAACTTCAGTATCATCGCAAGGTGGAGTTATTCAAG 120

QY 1579 GGTGTGTATACAGATGATTTTATGACATGTTGCTTAAGATTGAATCCGTTCTCTATTG 1638

Db 121 GCGTGTGACACACAGATGATTATGACCTGCTGAAGATTGAATTCACACTATTTATTTA 180  
QY 1639 CTGTGTGATTTGTCTGCAAAAGGAGAAATTTGGCAAGAAATGTATATCATCAAGCAT 1698  
Db 181 CTGTGTGATTTGTCTGCAAAAGGAGAAATTTGGCAAGAAATGTATATCATCAAGCAT 240  
QY 1699 GGAGAGTCCAGATTTCTGGAGGCTCTGATGCTGATGCTGATGCTGATGCTGATGCT 1758  
Db 241 GGAGAGTCCAGATTTCTGGAGGCTCTGATGCTGATGCTGATGCTGATGCTGATGCT 300  
QY 1759 GGGTCGGTGTGTTGGAGAAATCAGCTCTTAGCAGCAGGAGGAGAAACCGTGCAGTGGC 1818  
Db 301 G-----GCCCTTCTGGCAAGGAGGAGAAATCGCCGACAGCT 339  
QY 1819 AATGTGTGGGCCACCGGTTGGCCAAATCTTTTAACTCTAGACAAAGAACCTTCCAGAA 1878  
Db 340 GATGTTGTGGCCACGAGTTTGGCCAAATCTTTTAACTCTAGACAAAGAACCTTCCAGAA 399  
QY 1879 ATTCTAGTGCATTATCCAGATTTCTGAAGGATCCTCATGAGAAAGCCAGAGTGTCTTTA 1938  
Db 400 ATTCTGCTGCATTTATCCAACTTCTTAAAGCTCTCATGAGAAAGCCAAATTTCTTTTA 459  
QY 1939 AAGCAGAGGCTTAAGACCGCAGAACCAACCCCTCCAGAGAAAGATCTTTGCCCTCTCTTC 1998  
Db 460 AGCCAGAGGAGGAGAACCACTCAGGCAATCCCTGCAAGACCGAGCTGCTCTTTTTC 519  
QY 1999 CCACGAAAGAGAGACACCCCAACTGTTTAAACTCTCTAGGAGGACAGGAGAAAGCA 2058  
Db 520 CCACGAAAGAGAGACACCCCGAATGCTTAAAGTTCTCTTAGGACACACAGGAGGTGG 579  
QY 2059 AGCTTTCAGACTACTCAATTTGAAGCGAGGAGCAAGCAGCTCAG--AAGAAAGAAATTT 2116  
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QY 2117 CTGAAGGAGGAGAGGAGAGGAGAAAGAAATGAAGATAAAGAAAGAAATGAAGATA 2176  
Db 640 GTTCACAGGCAAGAAAGAGAGGAGGAGAAAGAAATTTGAAGACCAAGGAGACAGAGCTT 699  
QY 2177 AACAAAAAGAAATGAAGATAA 2198  
Db 700 AGCAGAAAAAGAGAAAAA 721

## RESULT 8

LOCUS BX401127 1054 bp mRNA linear EST 28-APR-2004  
DEFINITION BX401127 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens  
CDNA clone CSODK009YE13 5-PRIME, mRNA sequence.  
ACCESSION BX401127  
VERSION BX401127.2 GI:46846684  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1054)  
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On May 13, 2003 this sequence version replaced gi:30614460.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
7817-r

For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CSODK009AC07QPi&c=7817.r.

## FEATURES

Location/Qualifiers

## source

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/note="1st strand cDNA was primed with a NotI-oligo(dT)  
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digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 15.0%; Score 363.8; DB 5; Length 1054;  
Best Local Similarity 60.8%; Pred. No. 1.2e-73;  
Matches 611; Conservative 35; Mismatches 353; Indels 6; Gaps 5;  
QY 861 AAATGAGCTAAGGAAACACTACAGACTTCTTACAAAATTTCAAGTTGGATGCGCATCAAT 920  
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QY 921 AATACCAATTTGATATTTGCTACCTCTTCTTTGGGTTTAAATCAATGTTTAGAGCAAAATAG 980  
Db 64 CTTGCCCTTGGATTTTCTCTATTTTGAAGTCGGTGTGAACCCCTCTCCGCGYTCMCCG 123  
QY 981 GATGTTAAA--GTACACTTTCATTTTGAATTTTAAATCATCACCTAGAGCTCTATATGGAC 1038  
Db 124 CTGTTTAAATGATATCATGGCCCTTCTCGAGTTTAAACAGCCGCTGGATTCATCTCTCAGC 183  
QY 1039 AAAGCATATATCTACAGAGTTTATTCGAACAACCTGGATATTTGCTGTTTATTTCTGCACAT 1098  
Db 184 AAAGCTACGTGTACAGGTCATCAGGAYCACAGYTTACCTTCTVTACAGCTGCTCATTTG 243  
QY 1099 AATGCTGTGTTTATTTACTGGGCTTCAAACTATGAAGAAATGGCACTACTAGATGGGTG 1158  
Db 244 AATTCCTGTCTTTATTTACTGGGCATCGGCCCTTCAGGGCCTCGGCTCCACTCACTGGGTT 303  
QY 1159 TATCATGGGAGGAAAGACAGTATCTGAGATGTTTATTTATTTGGGAGTTTCGAACCTTTAAT 1218  
Db 304 TACGATGGGTGGGAAACAGTTATTTCTGCTGTGTACTCTTGTCTGTGAARACMCTCATC 363  
QY 1219 ACCATGCTGGCCCTTCAGAAACCAAACTTTATTTGAAATTTGTTTTCAACTCTTGAAT 1278  
Db 364 AYCATCGGGGGCTGCTGACCCCAAGAYACTTTTGAAATTTGTTTCCAGCTGTGTAAT 423  
QY 1279 TTTTTCCTGAGATTTTGTCTCTCCAGTTTAAATGCTGATGATGAGATGATGATGGA 1338  
Db 424 TATTTCAAGGCGCTTTTGTCTTCTGTGATGATTTGGACAGATGAKAGATGTTGGTAGGG 483  
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Db 484 GCCGCCACCG-CAGACAGACCTACTACCGAGCTGTCATGGACAGCAGCGTGAATGATCATG 542  
QY 1399 AACAAATTAATCTCCATTCCTTAACTTTGTGCAAAAGCGAGTTCCGAGCTTGGTATGAATATACA 1458  
Db 543 AATTTTACAAGATCCCAAGTCGTCGAGAACGAGTCAAGACTGGTGAAGATGACACC 602  
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QY      1758  TGGGTCGGTGTGGGAAATCAGCCCTTCTAGCAGCAGGAGGAGAAACCGTCGAATGC 1817
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QY      1818  CAAATGTTGGCCCGCCAGGGTTTGCCCAATCTTTTAACCTTAGACAA 1862
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RESULT 9
AA069559 468 bp mRNA linear EST 02-FEB-1997
zf75a04.r1 Soares pineal gland N3HPG Homo sapiens cDNA clone
IMAGE:382734 5', mRNA sequence.

ACCESSION AA069559
VERSION   AA069559.1 GI:1576971
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

REFERENCE
AUTHORS   Hillier,L., Lemon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
          Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W.,
          Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le.N.,
          Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
          Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
          Trevaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
          and Marra,M.
          Generation and analysis of 280,000 human expressed sequence tags
          Genome Res. 6 (9), 807-828 (1996)
          97044478
          8889549
          Contact: Wilton RK
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: est@watson.wustl.edu
          This clone is available royalty-free through LNL; contact the
          IMAGE Consortium (info@image.lnl.gov) for further information.
          Insert Length: 874 Std Error: 0.00
          Seq primer: -28M13 rev2 from Amersham
          High quality sequence stop: 382.

FEATURES
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/clone_lib="Soares pineal gland N3HPG"
/clone_Organ="pineal gland; Vector: pRTT3D (Pharmacia)
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1st strand cDNA was primed with a Not I - oligo(dT) primer
[5', TGTTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTTT
3'], double-stranded cDNA was size selected, ligated to
Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pRTT3
vector (Pharmacia). Library constructed by Bento Soares
and M.Fatima Bonaldo."

ORIGIN
Query Match 13.2%; Score 320.8; DB 1; Length 468;
Best Local Similarity 97.9%; Pred. No. 1.1e-63;
Matches 325; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1250  TATTTGAAATCTTTTCAACTCTTTGAATTTTTTTCTGGAGTTTTTGTCTTCAGTT 1309
Db      1  TCTTTGAAATCTCTTCCAGCTGCTGAATTTTTCACGGCGCTCTTTGCTTCTCTGTA 60

QY      1310  TAAATGGTCAGATGAGAGTGTGATTGGAGCGATACAGCCATCAGAACTTCCCGG 1369
Db      61  TGATCGACAGATGAGAGTGTGGTAGGGCGCCACCGCGGACAGACTACTACCGCA 120

QY      1370  CTTGATGATGATGACACCATTTGCTTACATGAACAAATTACTTCCATTCTTAACTTGTCAA 1429
Db      121  GTTGCATGACAGACGCGGTGAAGTACATGAATTTCTACAAGATCCCAAGTCGTCGAGA 180

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QY      19  AAAGTCAACAAGGTGAAGCCTATAGGAGAGAAACAATGAGAATGAACAAAGTTCTCGTCGG 78
Db      2  AAAGTCAACAAGGTGAAGCCTATAGGAGAGAAACAATGAGAATGAACAAAGTTCTCGTCGG 61

QY      79  AATGAAGAAGGCTCTCACCCAAAGTAATCAGTCTAGCAAAACACACAGCAGCAAGAAAC 138
Db      62  AATGAAGAAGGCTCTCACCCAAAGTAATCAGTCTAGCAAAACACACAGCAGCAAGAAAC 121

QY      139  AAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCTCAGTCACTCTTGAAGAGCCACAC 198
Db      122  AAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCTCAGTCACTCTTGAAGAGCCACAC 181

QY      199  ACCAATACATCAAGACAAACTCTTCCAAGAAAATTCCTCTGGAGATCTGACCAAAACCT 258
Db      182  ACCAATACATCAAGACAAACTCTTCCAAGAAAATTCCTCTGGAGATCTGACCAAAACCT 241

QY      259  GACCCCTCAAAATGACAGAGAACCACTGGAACAGTGCAGAGCAGAGCAAGAAATGACCCC 318
Db      242  GACCCCTCAAAATGACAGAGAACCACTGGAACAGTGCAGAGCAGAGCAAGAAATGACCCC 301

QY      319  GGGAAAGAGGTCTCAAAACAGCCCAACAAACAA 350
Db      302  GGGAAAGAGGTCTCAAAACAGTTCACCTAGAA 333

RESULT 10
BP224184
LOCUS     BP224184
DEFINITION ColP6731, mRNA sequence.
ACCESSION BP224184
VERSION   BP224184.1 GI:52097089
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 656)
          Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
          Mizushima-Sugano,J., Nakai,K. and Sugano,S.
          Sequence comparison of human and mouse genes reveals a homologous
          block structure in the promoter regions
          Genome Res. 14 (9), 1711-1718 (2004)
          Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1..656
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="ColP6731"
/clone_lib="Sugano cDNA library, colon mucosa"

ORIGIN
Query Match 13.2%; Score 320.8; DB 5; Length 656;
Best Local Similarity 69.1%; Pred. No. 1.2e-63;
Matches 453; Conservative 0; Mismatches 202; Indels 1; Gaps 1;

QY      1250  TATTTGAAATCTTTTCAACTCTTTGAATTTTTTTCTGGAGTTTTTGTCTTCAGTT 1309
Db      1  TCTTTGAAATCTCTTCCAGCTGCTGAATTTTTCACGGCGCTCTTTGCTTCTCTGTA 60

QY      1310  TAAATGGTCAGATGAGAGTGTGATTGGAGCGATACAGCCATCAGAACTTCCCGG 1369
Db      61  TGATCGACAGATGAGAGTGTGGTAGGGCGCCACCGCGGACAGACTACTACCGCA 120

QY      1370  CTTGATGATGATGACACCATTTGCTTACATGAACAAATTACTTCCATTCTTAACTTGTCAA 1429
Db      121  GTTGCATGACAGACGCGGTGAAGTACATGAATTTCTACAAGATCCCAAGTCGTCGAGA 180

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QY 1430 ACCGAGTTGGGACTTGGTATGATATATCATGGGACTCTCAAGAAATGCTAGATGAGTCTG 1489  
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 Db 181 ACCGCGTCAAGACACTGGTACGAGTACACCTGGCACTCGCAAGGATGCTGGATGAGTCAG 240  
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 QY 1490 ATTTGCTTAAGACCTACCACTACGCTGCTAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 1549  
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 Db 241 AGCTGATGGTGAGCTTCCAGACAAGATGCGGCTGGACCTCGCCATCGACGTGAATCTACT 300  
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 QY 1550 GCATCATCAGCAAAAGTCGACTTGTTCAGGGTGTGTATACACAGATGATTTATGACATGT 1609  
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 QY 1610 TGCTAAGATTGAATTCGCTTCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1669  
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 Db 361 TGAAGAGCTTTCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
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 QY 1670 TTGGCAAGAAATGATATATCATCAAGCATGAGAGTCCAAAGTCTTGGAGCCCTGATG 1729  
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 Db 421 TCGGCGGTGAGATGATCATATCCAGGCGAGGCAAGTGCAGGTCTTGGCGGCGGCTGATG 480  
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 QY 1730 GTACTAAAGTCTGCTTACTCTGAAAGCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1789  
 |||||  
 Db 481 GGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
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 QY 1790 CAGCAGGAGGAGAAACCGTCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1849  
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 Db 541 CTGTTGGGGGGGAAACCGGCGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 600  
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 QY 1850 TAACTCTAGACAAAGAACCTCCAG--AAATTCAGTGCATATTCAGATCTCGA 1904  
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 Db 601 TCATCCTGGATGAAGAGGACCTGAATGAAATTTTGGTGCATATTCCTGAGTCTCA 656  
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## RESULT 11

BQ068992  
 LOCUS BQ068992 978 bp mRNA linear EST 02-APR-2002  
 DEFINITION AGENCOURT\_6740166 NIH\_MGC\_47 Homo sapiens cDNA clone IMAGE:5802872  
 5', mRNA sequence.  
 ACCESSION BQ068992  
 VERSION BQ068992.1 GI:19898038  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 978)  
 NIH-MGC <http://mgi.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-romail.nih.gov](mailto:cgapbs-romail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LICM2037 row: p column: 09  
 High quality sequence stop: 726.  
 Location/Qualifiers  
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 /clone="IMAGE:5802872"  
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 /clone\_lib="NIH\_MGC\_47"  
 /note="Organ: brain; Vector: pOTB7; Site: 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'

## FEATURES

## source

## RESULT 12

CK619966  
 LOCUS CK619966 633 bp mRNA linear EST 26-JAN-2004  
 DEFINITION mk30e03.y1 Mouse retina, unamplified: mk/ml Mus musculus cDNA clone  
 mk30e03 5', mRNA sequence.  
 ACCESSION CK619966  
 VERSION CK619966.1 GI:41340852  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 633)  
 Ida, H., Boylan, S., Weigel, A., Smit-McBride, Z., Chao, A., Gao, J.,  
 Buchoff, P., Wistow, G. and Hjelmeland, L.  
 Expressed sequence tag analysis of mouse retina  
 TITLE

adaptor: GGCACGAG (G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 12.7%; Score 308.4; DB 5; Length 978;  
 Best Local Similarity 67.7%; Pred. No. 9.9e-61;  
 Matches 432; Conservative 0; Mismatches 206; Indels 0; Gaps 0;  
 QY 1326 AGATGTGATGGAGAGCTACAGCAATCAGAACTACTTCCGCGCTGCATGGATGACAC 1385  
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 Db 1 AGATGTGATGGGCGCGCCACCGGGGAGACACCTACTTACCGCAGCTGCATGGACAGCAC 60  
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 QY 1386 CATTGCCCTACATGAACAACTTACTCCATTCCTAACTTGTGCAAAAGCGAGTTCGAGCTTG 1445  
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 QY 1446 GTATGAATATACATGGGACTCTCAAGAATGCTAGATGAGTCTGATTTTGTCTTAAGACCTT 1505  
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 Db 121 GTACGAGTACACCTGGCACTCGCAAGCATGCTCGATGAGTCAAGCTGATGGTGCAGCT 180  
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 QY 1506 ACCAACTACGGTCCAGTTAGCCCTCGCCATTGATGTGAATTCAGCATCATCAGCAAAAGT 1565  
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 Db 181 TCCAGACAAGATGCGGCTGGACCTCGCATCGAGCTGAACCTACAACATCGTTAGCAAAAGT 240  
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 QY 1566 CGACTTGTTCAGGGTGTGTATACAGATGATTTATGACATGTTTGTAAATTCGAAATC 1625  
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 Db 241 CGCACTCTTTTACGGGCTGTGACCGGCGAGATGATCTTTGACATGCTGAAGAGGCTTCGCTC 300  
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 QY 1626 CGTTCTCTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1685  
 |||||  
 Db 301 TGTGCTTACTGCTGCCAAGCATGCTGTCAGAGAGGGGAGATCGGCCGTGAGATGTA 360  
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 QY 1686 TATCATCAAGCATGGAGAAAGTCCAAGTCTTTGGAGGCCCTGATGCTACTAAAGTTCGTGT 1745  
 |||||  
 Db 361 CATCATCCAGCAGGCGCAAGTGCAGGTCTTTGGGCGGCCCTGATGGGAAATCTGTGCTGT 420  
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 QY 1746 TACTCTGAAAGCTGGTTCGGTGTGAGAAATCAGCTTCTAGCAGCAGGAGGAGGAAA 1805  
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 Db 421 GACGCTGAAAGCTGGATCTGTGTTTGGAGAAATAAGCTTGTGCTGTGTTGGGCGCGGAA 480  
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 QY 1806 CCGTGCAGAACTGCCAATGCTGTGGCCACCGGTTTGGCCAAATCTTTTAACTCTAGACAAAAA 1865  
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 Db 481 CCGCGCGACGCCCAACGTTGTTGGCGCACGGGTTTACCACCTCTTCTCTCTGGATAGAA 540  
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 Db 541 GGACCTGAATGAGATTTTGGTGCATTTCTGAGTCTCAGAAAGTTACTCCGGAAGAAAGC 600  
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 Db 601 CAGCGCATCTGTGAGAGCAACCAATAAGCCCAAGGAGG 638  
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JOURNAL  
COMMENT

Unpublished (2004)  
Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov  
Plate: 30 row: e column: 03  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
1. .633  
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/clone\_lib="Mouse retina, unamplified: mk/ml"  
/notes="Organ: Eye; Vector: pSPORT1; 270ug total RNA was extracted from 200 adult male mouse retinas. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (<http://www.lifetech.com/>). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGACGTAGTCTAGATCGCGGGCGGCC(7)15-3']. cDNA was cloned in Not I/Sal I sites. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 12.5%; Score 304; DB 7; Length 633;  
Best Local Similarity 67.6%; Pred. No. 9.7e-60;  
Matches 427; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 1315 GGTGAGATGAGATGTTGAGAGAGCTTACAGCCAAATGACATCTTCCATTCCTAACTTGTGCAAAAGCGA 1434  
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QY 1375 ATGATGACACCATTCCTACATGACAAATTAATCTCCATTCCTAACTTGTGCAAAAGCGA 1434  
DB 61 ATGGACAGCACAGTGAAGTACATGAATCTTCAAGATCCCGAGGCTGTGTCAGAACCCGT 120

QY 1435 GTTCGGACTTGGTATGAATATACATGGGACTCTCAAGAAATGCTAGATGAGTCTGATTTG 1494  
DB 121 GTCAAGACCTGGTATGAGTACACTTGGCATTCGCAAGGCATGCTGGATGAGTCAGAGCTG 180

QY 1495 CTTAAGACCTTACAACTACGTTCCAGTTAGCCCTCGCCANTGATGTGAATTCAGATC 1554  
DB 181 ATGTTACAACTTCGGACAAAGATGCGACTGACCTGGCATTCGCGCCATTGATGTGAATTCAGTATT 240

QY 1555 ATCAGCAAGTCAGCTGTTTCAAGGGTTGTGATACACAGATGATTATGACATGTTGCTA 1614  
DB 241 GTCAGCAAGTGGCCCTCTTTCAAGGGCTGTGACCGGACAGATGATTCGACATGCTCAAG 300

QY 1615 AGATTGAAATCCGTTCTCTATTTCCTGTTGACTTTGTCTGCAAAAGGGAGAAATTTGGC 1674  
DB 301 CGGCTTCGTTCTGTTGTCTACCTACCCATGACTATGTGTGCAAGGGGAGATTGGC 360

QY 1675 AAGGAAATGATATCATCAAGCATGAGAGAGTCCAAAGTCTTGGAGGCCCTGTAGTACT 1734  
DB 361 CGAGATGATACATTATCCAGCGGGGCGAGTGCAGTGTGCGGGCGGCCAGATGGGAAG 420

QY 1735 AAGTTCTGTTACTCTGAAAGCTGGTGGTGTGTTGGAGAAATCAGCTTCTAGCAGCA 1794  
DB 421 GCTGTACTGTGACACTCAAGCCGGATCGGTGTTTGGAGAAATTAAGCTTGTGCTGTGTC 480

QY 1795 GGAGGAGGAAACCGTCCAACTGCGATGTTGGGCCCGCCAGGGTTTCCCAATCTTTTAACT 1854  
DB 481 GGGGGTGGCAACCGGCGCACAGCAACGTTGGTGGCCCATGGCTTACCAACCTCTTTCATA 540

QY 1855 CTAGACAAAGAACCTCCAGAAATTTAGTGCATTATTCAGATTTCTGAAGGATCCTC 1914  
DB 541 CTGGCAAGAGGACTTGAATGAATTTTGTGCTTACCGGAATCTCAGAGTTACTT 600

QY 1915 ATGAAGAAAGCCAGAGTGTCTTTTAAAGCAGAA 1946  
DB 601 CGAAGAGCCAGCGGCGATGCTAAGAAATAA 632

RESULT 13  
AUI37778

LOCUS AUI37778 PLACE1 Homo sapiens cDNA clone PLACE1007225 5', mRNA

DEFINITION sequence.

ACCESSION AUI37778

VERSION AUI37778.1 GI:10999299

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 694)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, I.

TITLE HRI human cDNA project

JOURNAL Unpublished (2000)

COMMENT Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: [genomics@hri.co.jp](mailto:genomics@hri.co.jp)  
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.  
Location/Qualifiers  
1. .694  
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/note="Vector: pME18SFL3"

ORIGIN

Query Match 12.4%; Score 301.4; DB 1; Length 694;  
Best Local Similarity 66.3%; Pred. No. 4e-59;  
Matches 445; Conservative 0; Mismatches 225; Indels 1; Gaps 1;

QY 1049 TCTACAGAGTTATCGAACAACTGGATCTTCTGTTTATTTGTCACATTAATGCTGTG 1108  
DB 20 TCTGAGGGTCAATCAGGACCAAGCCCTACCTTCTCTACAGCTTGAATTTCTGTCT 79

QY 1109 TTTATTACTGGGCTTCAAACTATGAAGGAATTTGGCACTACTAGATGGGTGTATGATGGG 1168  
DB 80 TTTATTACTGGCATCGGCTATCAGGGCTCGGCTCCACTCAGTGGGTTTACGATGGCG 139

QY 1169 AAGGAAACGAGTATCTGAGATGTTATTTATTTGGGAGTTTGAACCTTTAATCAGATGGTG 1228  
DB 140 TGGGAAACAGTTATATTCGCTTACTTCTTACTTGTGTGAAGACCCCTCATCACCATCGGG 199

QY 1229 GCCTTCCAGAACCAAACTTTTATTGAAATTTTTCCTCAACTCTTGAATTTTTTTCTG 1288  
DB 200 GGCTGCTGACCCCAAGACACTCTTTTGAATTTGTTTCCAGCTGCTGAATTTATTCACGG 259

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 BX104558.1 GI:27832995  
 EST.  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 741)  
 Ebert,L., Heil,O., Hennig,S., Neubert,P., Pattsch,E., Peters,M.,  
 Radelof,U., Schneider,D. and Korn,B.  
 Human Unigeneset - RZPD3  
 Unpublished (2003)  
 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD; IMAGp998p13890.  
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
 Human Unigeneset - RZPD3 (RZPDLIB No.972)  
[http://www.rzpd.de/CloneCards/cgi-](http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi?response?libNo=972)  
[bin/showlib.pl.cgi?response?libNo=972](http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi?response?libNo=972) Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de  
 This clone is available royalty-free from RZPD;  
 contact RZPD ([clone@rzpd.de](mailto:clone@rzpd.de)) for further information. Seq primer:  
 M13r, Primer sequence: TTTCACACAGGAACAGCTATGAC.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="IMAGp998p13890 ; IMAGE:384252"  
 /tissue type="brain, pineal gland"

FEATURES	SOURCE
1. <b>High Accuracy:</b> The model achieves a high accuracy rate, indicating its effectiveness in predicting the target variable.	Model Performance Metrics
2. <b>Robustness:</b> The model demonstrates robustness against various input variations and noise, ensuring reliable predictions.	Model Performance Metrics
3. <b>Interpretability:</b> The model's predictions are interpretable, allowing users to understand the underlying factors influencing the outcome.	Model Performance Metrics
4. <b>Scalability:</b> The model is scalable, capable of handling large volumes of data and complex tasks efficiently.	Model Performance Metrics
5. <b>Real-time Processing:</b> The model is designed for real-time processing, enabling immediate decision-making based on incoming data.	Model Performance Metrics
6. <b>Customization:</b> The model is highly customizable, allowing users to tailor it to specific requirements and datasets.	Model Performance Metrics
7. <b>Integration:</b> The model seamlessly integrates with existing systems and workflows, facilitating easy adoption and deployment.	Model Performance Metrics
8. <b>Security:</b> The model adheres to strict security protocols, ensuring that data is protected and privacy is maintained.	Model Performance Metrics
9. <b>Flexibility:</b> The model is flexible, capable of adapting to changing requirements and evolving data patterns.	Model Performance Metrics
10. <b>Cost-effectiveness:</b> The model is cost-effective, providing high performance at a reasonable price point.	Model Performance Metrics

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Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Query Match      11.6%; Score 280.8; DB 4; Length 738;
Best Local Similarity 63.0%; Pred. No. 2.6e-54;
Matches 466; Conservative 0; Mismatches 272; Indels 2; Gaps 2;

QY 748 ATACACTACTGGCTTATTGGGACATCATATGTGATATCATCTTACCTTTATGATATGCTA 807
DB 1 ATCCACTTCTGGCTCCTCATGGATTACTTGTGGACTTCACTTACCTCTGGACATCACC 60

QY 808 TTATTCAGCCAGACTCCAGTTTGTAAAGAGGAGGACATAATAGTGGATTCAAAATGAG 867
DB 61 GTGTTCCAGATGGCCCTGCAG-TTGTCAAAGGGGGGACATCATACAGACAAGAGGAG 119

QY 868 CTAAGGAAACACTACAGAGCTTCTACAAAATTTTCAGTTGGATGTCGCATCAATAATACCA 927
DB 120 ATGCGTAATAACTACCTGAAAGTCTCGCCGGTTTAAAGATGGACCTGCTCTGCCCTCCTGCC 179

QY 928 TTTGATATTGCTACCTCTTCTTTGGGTTTAAATCCAAATGTTTAGAGCAATAGATGTTA 987
DB 180 TTGGACTTCTCTACTTGAACCTTGGCATCAACCCCTCTCTTGGCTGCCCGCTGCCGTG 239

QY 988 AAGTACACTTCAATTTTGAATTAATCATCACTAGAGTCTATAATAGGACAAAGCATAT 1047
DB 240 AAGTACATGGCTTCTTTGAGTTTAAATAACCGCTTGAAGCCATCTCTCAGCAAAAGCCTAC 299

QY 1048 ATCTACAGAGTTATTGAAACAACTGGATCTTGGCTGTTTATTTCTGCACATTAATGCCGT 1107
DB 300 GTTTACAGAGTCACTACAGACCGGCTTACCTGCTGTACAGCCCTGCACCTCAACTCCTGC 359

QY 1108 GTTTATTACTGGCTTCAAACCTATGAAGAAATGGCACTACTAGATGGGTGTATGATGGG 1167
DB 360 CTTTACTACTGGGATCAGCCT-TCCAGGATCGGCTCCACTCAGTGGGTTTACGACGGA 418

QY 1168 GAAGGAAACGAGTATCTGAGATGTTATTAATGGGAGTTCGAACTTTTAATTACCATTTGT 1227
DB 419 GTGGGAAACAGTTATATTCGATGCTACTACTGGGCTGTGAAACCCCTCATCACCATCGGA 478

QY 1228 GGCCTTCCGAAACCAAACTTTTATTTGAATTTGTTTTCAACTCTGAAATTTTTTTCT 1287
DB 479 GGACTGCCCGACCCCGACGCTCTTTGAGATTGCTTCCAGCTGTGAACTATTTTACC 538

QY 1288 GGAGTTTTTTGTTCTCCAGTTTAAATTTGGTCAGATGAGAGATGTGATTGGAGCAGCTACA 1347
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QY 1348 GCCAATCAGAACTACTTTCGGGCTCGATCGATGACACCATTCCTTACATGAACAATTAC 1407
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QY 1408 TCCATTCTTAACTTGTGCAAAAGCGAGTTTCGACCTTGGTATGAATATACATGGACTCT 1467
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QY 1468 CAAAGAATGCTAGATGAGTC 1487
DB 719 CAAGGCATGCTGATGAGTC 738
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